GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

July 11, 2003, 10:51:49; Search time 18 Seconds (without alignments)
1863.940 Million cell updates/sec

Title:
US-09-654-652A-3
Sequence:
1824
Sequence:
1 MNIKKTAVKSALAVAAAAAA......AKGAKVNPNGHKRYRVNFEH 349
Scoring table:
Gapop 10.0, Gapext 0.5
Searched:
283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters:
283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	. 12	11	10	9	8	7	6	ъ	4	w	2	–	No.	Result
149	154.5	157.5	159.5	164	170.5	172.5	173	173	180.5	189.5	190.5	197	206	206	221	224.5	227.5	228	230	233.5	237	242.5	242.5	247.5	248	265.5	8	œ	Score	
8.2						9.5					10.4	10.8	11.3	•	12.1	•				٠	13.0	•			ω ·	14.6	14.7	100.0	Match	Query
289	277	269	287	286	282	277	642	282	268	467	302	269	289	263	246	242	238	237	507	243	334	802	239	276	242	252	851	349	Length	
2	N	N	N	N	N	2	ν	N	N	N	N	N	N	N	N	N	ب ــا	_	N	٢	_	N	_	ν	_	N	ν	ν	- BB	
T06166	S71222	S61555	T04236	S71225	A85354	B85354	B72428	T02354	S34804	S30839	G84053	н95976	C98231	AB3055	D97245	JS0611	S19012	S11927	S64507	S15388	S23498	A36910	A29091	I40453	LXBS	A48378	H84053	A44507	ID	
endot	endo-	endo-	xyloglucan endo-1,	en		hypothetical prote	laminarinase - The	œ.	protein -	UTR2 protein - yea	d-endo-	endo-beta-1,3-1,4-	1,3-1,	1,3-1,4	1,3(4	-beta	licheninase (EC 3.		mbran	(E)	cheninase (EC	eta(1	OEC	(EC	_	e (EC	-1,3-1,	nase (EC	Description	

RESULT 2

#84053
endo-beta-1,3-1,4 glucanase (licheninase) bglS [imported] - Bacillus halodurans (strz C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H84053

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4 4	43	42	41	40	39	38	37	36	35	34	33	32	ω	30
128	128	128.5	128.5	129.5	131.5	132	133.5	137	138	139.5	140.5	145	145.5	146.5
7.0	7.0	7.0	7.0	7.1	7.2	7.2	7.3	7.5	7.6	7.6	7.7	7.9	8.0	8.0
848	283	292	277	1.324	301	295	286	292	422	286	280	305	310	284
N	b	N	N	Ŋ	N	Ν	Ν	N	2	N	2	N	2	N
B97454	T07678	T04514	JE0156	T18265	C87296	T10210	S48201	T06201	S48564	T06202	T02090	G84568	A86239	T52097
hypothetical prote	xyloglucan endo-1,	xyloglucan endo-1,	end-xyloglucan tra	endo-1,3(4)-beta-g	beta-glucanase [im	xyloglucan endo-1,	licheninase (EC 3.	<pre>xyloglucan endo-1,</pre>	probable membrane	xyloglucan endo-1,	xyloglucan endo-1,	probable xylogluca	protein T10024.17	xyloglucan endo-1,

ALIGNMENTS

Оу	Оy	Db Qy	ОУ	Qу	Оy	Query M Best Lo Matches	A; Refer A; Acces A; Statu A; Molec A; Resic A; Cross C; Keywo	A4450/I i A4450/I ilcheninase C;Species: i C;Date: 03-1 C;Accession R;Teather, I J. Bacteriol A:Title: NV
301 PPSSSSATIAIHGMRTTPAVAKEHRNLVNAKGAKVNPNGHKRYRVNFEH 349 	241 YSRDGMLIIALTRKGQESFNGQVPRDDEPAPQSSSSAPASSSSVPASSSSVPASSSSAFV 300 	181 PLEQEINWVKVYKYTPGQGEGGSDETLDWTDNEDTEDGSRWGKGDWTEDGNRVDLTDKNI 240 	121 FHTYGLEWIFNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKL 180 	61 SMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQA 120 	1 MNIKKTAVKSALAVAAAAAAITTNVSAKDESGAELYTLEEVQYGKFEARMKMAAASGTVS 60 	Query Match 100.0%; Score 1824; DB 2; Length 349; Best Local Similarity 100.0%; Pred. No. 1.5e-122; Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Reference number: A44507; MUID:90299807; PMID:2193918 A;Recession: A44507 A;Retus: preliminary A;Status: preliminary A;Molecule type: DNA A;Residues: 1-349 <tea> A;Residues: 1-349 <tea> A;Cross-references: EMBL:M33676; NID:g148575; PIDN:AAA24896.1; PID:g148576 C;Keywords: glycosidase; hydrolase; polysaccharide degradation</tea></tea>	
<i>Y</i>								

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A; Note:
C; Superf
C; Keywor
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C;Date: 01-Dec-1993
C;Accession: A48378
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Appl. Microbiol. Biotechnol. 38, 507-513, 1993
A;Title: Characterization, cloning and sequencing of a thermostable endo-(1,3-1,4) beta
A;Reference number: A48378; MUID:93159752; PMID:7763386
A;Accession: A48378
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A;Molecule type: nucleic acid
A;Residues: 1-252 <LOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             licheninase (EC 3.2.1.73) - Bacillus brevis N; Alternate names: lichenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-851 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Bacillus brevis
Date: 01-Dec-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   Note: sequence extracted from NCBI backbone (NCBIN:124672, NCBIP:124673) Superfamily: licheninase
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Best Local
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es 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                             glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                         GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQ 140
                                                                    EGGQVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 196
                                                                                                                 GKDTTRIQFNYFTNGVGG----NEEYYDLGFDASESFNTYAFEWREDSITWYVNGEAVHTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVRKTEGGQVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP-- 196
                                                                                                                                                                                                        SARNYKAGELRTNDFYHYGLFEVSMKPAKVEGTVSSFFTY-TGEWDWDGDPWDEIDIEFL 148
                                                                                                                                                                                                                                                  SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRVDLT -- DKNIYSRDGMLILALTRKGQESFNGQVPRDDEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALDEEESGDDNEEEPVEEVEEEPAEDEEVSVRPIGSAIYETFNTFNEDIWSIAHGWT-NG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVHTA----TENIPQTPQKIMMNLWPGVGVDEWTGVFDGDNTPLHADYEWV----RYTPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIEFLGKDTTRIQFNYFTNGVGG---NEFYYDLGFDASESFNTYAFEWREDSITWYVNGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEV
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                       -TENIPQTPQKIMMNLWPGVGVDGWTGVFDGDNTPVT5; FDWV---RYTP
                                                                                                                                                                                                                                                                                                                                                                                         hydrolase; polysaccharide degradation
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sequence of the alkaliphilic bacterium
50; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                       14.6%;
35.8%;
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                                                                                                                                                                                                                                                                                                                       Score 265.5; DB 2
Pred. No. 9.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 268.5; DB 2
Pred. No. 2.6e-11;
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                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-Nov-1994 #text_change 07-May-1999
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                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DNFDTFDGSRWG-KGDWTFDG 230
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                         251
                                                                                                                                                                                                                                                                                                 Gaps
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C; Superfamily: licheninase
C; Keywords: extracellular p
F; 1-28/Domain: signal seque
                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-23, 'S', 25-82, 'S', 84-242 <TEZ>
A; Cross-references: DDBJ:D00518; NID:g216243;
A; Experimental source: strain Y-25, clone pLE1
R; Yuuki, T; Tezuka, H; Yabuuchi, S.
Agric. Biol. Chem. 53, 2341-2346, 1989
                                                                  A; Description:
                                                                                       C; Function:
                                                                                                                                 C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X00754; NID:g3981
A;Experimental source: strain C120
A;Note: the authors translated the codon C
R;Tezuka, H.; Yuuki, T.; Yabuuchi, S.
Agric. Biol. Chem. 53, 2335-2339, 1989
A;Title: Construction of a beta-glucanase
                                                                                                                 A;Gene:
                                                                                                                                                         A; Note: source was hyperproducing strain HL-25 with gene in A; Note: the amino ends of the mature forms of E-1 and E-2
                                                                                                                                                                                                          A; Contents: annotation
                                                                                                                                                                                                                             A;Title: Purification and some properties of two enzymes from a beta-glucanase hyperp
A;Reference number: A90027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-203, 'L', 205-242 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A90026
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extracellular protein; glycosidase;

sequence #status

predicted

hydrolase; <SIG>

polysaccharide degradation

catalyzes the

hydrolysis of 1,4-beta-D-glucosidic bonds in lichenin

from strain Y-25

are pyroglutamic

acid

A90026

בי:9216243; PIDN:BAA00405.1; clone pLE100

PID: 921624

NID: g39818; PIDN: CAA25328.1; PID: g685236

sites

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excreted

CAA

for residue 29

as

Lys and CCA

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hyperproducing

Bacillus

subtilis

using

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A; cross-references: GB:Z99124; GB:AL009126; NID:g2636442; A; Experimental source: strain 168 R; Murphy, N.; McConnell, D.J.; Cantwell, B.A. Nucleic Acids Res. 12, 5355-367, 1984 A; Title: The DNA sequence of the gene and genetic control: A; Reference number: A93526; MUID:84272222; PMID:6087283 A; Accession: A22914 A; Molecula trans-----
                                                                                                                                                                                                                                                                                                                                                                                                                                       A: Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferriari, Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarrevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T. M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Schikawa, H.; Danchin, A.; Areference number: A69380; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-242 < KUND A;Cross-references: GB:Z99124; GB:AL009126; NID:92636442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:246862; NID:g599673; PIDN:CAA86922.1; PID:g599674
R;KUNSt, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; BeC.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Genes encoding xylan and beta-glucan hydrolysing A; Reference number: I40370; MUID:95219081; PMID:7704256 A; Accession: I40370
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C;Date: 30-Jun-1988 #sequence_revision 13-Mar-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-242 < RES>
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RESULT 6
A29091
licheninase
                                                                                                           R; Hofemeister, J.; Kurtz, A.; Borriss, R.; Gene 49, 177-187, 1986
A; Title: The beta-glucanase gene from Bacil
                                                                                                                                              licheninase (EC 3.2.1.73) beta - Bacillus W;Alternate names: 1,3-1,4-beta-D-glucan C;Species: Bacillus amyloliquefaciens C;Date: 10-Sep-1999 #sequence_revision 10 C;Accession: A29091 R;Hofemeister, J.; Kurtz, A.; Borriss, R.
                               A; Reference number: A91564;
A; Accession: A29091
A; Molecule type: DNA
A; Residues: 1-239 <HOF>
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A;Title: Cloning and DNA sequencing of bgaA, a gene encoding A;Reference number: I40453; MUID:94288605; PMID:7517127
A;Accession: I40453
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
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Licheninase (EC 3.2.1.73) -
C; Species: Bacillus sp.
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A; Residues: 1-276 <RES>
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Matches
                   Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                      VSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 196
                                                                                                                                                                                                                                                                                                                                                                                                             TKIQFNYFTNGVGG---NEHYHELGFDAADDFNTYAFEWRPESIRWFVNGELVHTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YKAGELRTNDFYHYGLFEVSMKPAKSTGTVSSFFTY-TGPWDWENDPWDEIDIEFLGKDT
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                   GB:M15674;
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36.1%;
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MUID:87192007; PMID:3106158
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NID:g143009;
BE20/78
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a-D-glucan 4-glucanohydrolase;
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                                                                                                                                                                                   10-Sep-1999
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), 1.5e-10;
75;
                                                                                                                                                  Knowles, J.
                 PIDN: AAA87323.1;
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                 PID:g143010
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A36910
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A;Gene: bglA
C;Superfamily: licheninase
C;Keywords: glycosidase; hj
                                                                                                                    C;Species: Clostridium thermocellum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: $23498; $22317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:S61204; NID:g385910; PIDN:AAB26620.1; PID:g385911
A;Note: sequence extracted from NCBI backbone (NCBIN:131871, NCBIP:131872)
C;Superfamily: endo-1,4-beta-xylanase homology; Thermotoga xylanase A amino-terminal F;42-239/Domain: endo-1,4-beta-xylanase homology <XXI>
F;259-401/Domain: Thermctoga xylanase A amino-terminal repeat homology <TXA>
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             A; Reference number: A; Accession: S23498
                                                                                     R;Schimming, S.; Schwarz, W.H.;
Eur. J. Biochem. 204, 13-19, 199
                                                                                                                                                                                 licheninase (EC 3.2.1.73) licB precursor - Clostridium thermocellum N;Alternate names: beta:1,3-1,4-glucanase licB; lichenase licB
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A; Residues: 1-802 <FLI>
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                                                                                                                                                                                                                                                                                                                                                                                         GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                YSGGEFRTNNFYHYGYYECSMQAMKNDGVVSSFFTYTGPS---DDNPWDEIDIEILGKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSETADGRPWVEVDIEVLGKNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHTATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYDWMRYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                TQDIPKTPGKIMMNAWPGLTVDDWLKAFN-GRTPLTAHYQWVTYNK
                                                                                                                                                                                                                                                                                                                                   VSNLTGTQG-:LRENLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFLGKDTTKVQFNYYTNGAG----NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE----GTPWDEIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                   S23498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hydrolase; polysaccharide degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.3%;
                                                                    Clostridium thermocellum gene licB
                                 MUID:92155194; PMID:1740123
                                                                                       н.; Staudenbauer,
1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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                                                                                                                                                                                                                                                                                                                                                                        EKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 242.5; DB 2
Pred. No. 1.7e-09;
1; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 242.5;
Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -Nov-1994 #text_change
                                                                                                           W.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                              #text_change
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                                                                        and
                                                                                                                                                                                                                                                                                                                                   193
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                                                                                                                                                10-Sep-1999
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                                                                        encoded beta-1,3
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690

89

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RESULT 9
$15388
licheninase (EC 3.2.1.73) - Bacillus licheniformis
N;Alternate names: endo-beta-1,3-1,4-D-glucanase; lichenase
C;Species: Bacillus licheniformis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_chr
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                                                                                                                                                                                                                                                           A;Residues: 1-243 <LLO>
A;Cross-references: EMBL:X57279; NID:g39558; PIDN:CAA40547.1; PID:g39559
C;Superfamily: licheninase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1-27/Domain: signal sequence #status predicted <SIG>F;28-334/Product: licheninase #status predicted <MAT>F;273-296/Domain: Clostridium cellulase repeat homologyF;308-331/Domain: Clostridium cellulase repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-334 <SCH>
A;Cross-references: EMBL:X63355; NID:g40697; PIDN:CAA44959.1; PID:g40698 C;Genetics: A;Gene: licB
A;Gross-references: EMBL:X63355; NID:g40697; PIDN:CAA44959.1; PID:g40698 C;Genetics: A;Gene: licB
C;Superfamily: licheninase licB; Clostridium cellulase repeat homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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                                                                                                                                                                                                                                                                                                                                                               Eur. J. Blochem. 197, 337-343, 1991
A;Title: Molecular cloning, expression and nucleotide sequence A;Reference number: S15388; MUID:91224124; PMID:2026156
A;Accession: $15388
                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession:
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F;308-331/Domain:
                                                                                                                                                                                                                                                                                                                                  A; Molecule
                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                  Local
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                                                                                                                                                    TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                               RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                               TSPSYNKFDCGENRSVQTYGYGLYEVNMKPAKNVGIVSSFFTYTGPT---DGTPWDEIDI
KHTATTQIPQTPGK--IMMNLWNGAGVDEWLGSYN-GVTPLSRSLHWVRYTK
                                                              EFLGKDTTKVQFNYYTNGVG----NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-L
                                                                                             EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWTFDGNRVDLTDKNIYSR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIVSSFFTYTGPS---DNNPWDEID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEFLGKDTTKVQFNWYKNGVGG----NEYLHNLGFDASQDFHTYGFEWRPDYIDFYVDGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPTPTPTIAPSTPTNPNLPLKGDVNGDGHVNSSDYSLFKRYLLRVIDRFPVGDQS----VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-GRTPLQAEYEYVKYYPNGVPQD
                                                                                                                                                                                                  Conservative
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Pred. No. 1.4e-09;
                                                                                                                                                                                                                Score 233.5;
Pred. No. 1.
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                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                 1.7e-09;
ches 77;
                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                Length 243;
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242
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                                                                             A; Molecule type: DNA
A; Residues: 1-237 <BOR>
                                                                                                                             A; Reference number: A; Accession: S11927
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                                                                                                                                                                                                                Accession: S11927
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probable membrane protein YGR189c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G7553
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: S64507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross·references:
A;Map position: 7R
C;Keywords: transmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-507 <ARR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Arroyo, J.; Garcia-Gonzalez, M.; submitted to the Protein Sequence I A; Reference number: S64499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S64507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z72974; NID:g1323335; PID:e243566; PID:g1323336; GSPDB:GN000
                                                                                                                                                                                   172 V-GQFDESKLPLFQFINWVKYYKYTPGQGEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 TAVKSALAVAAAAALTINVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
SSSSVPASSSSAFVPPSSSSATNA
                                                                                          NRVDLTDKNIYSRDGMLILALTRKG--QESFNGQVPRDDEPAPQSSSSAPASS--SSVPA
                                                                                                                                                                                                                                       LDWAMDKTTWYLDGESVR----
                                                                                                                                                                                                                                                                         LEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQG------LRFNLWSS----ESAA----W
                                                                                                                                                                                                                                                                                                                                    SDDLD---
                                                                                                                                                                                                                                                                                                                                                                              QNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYG
                                                                                                                                                                                                                                                                                                                                                                                                                            TDLKHAGEIKYGSDGLSMTL-AKRYDNPSLKSNFYIMYGKLEVILKAANGTGIVSSFYLQ
                                                                                                                                         AGGETNYNDAPFTMYIEKVIVTDYSTGKKYTYGDQSGSW-ESIEADGGSIYGRYDQAQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane #status predicted <TMM>
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                                              -DFAVLANGGSISSSTSSSTVSSSASSTVSSSVSSTVSSSASSTVSSSVSSTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 230; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
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                                                                                                                                                                                                                                       -VLSNTSSEGYPQSPMYLMMGIWAGGDPDNAAGTIEW
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7.5e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanchez-Perez, M.; Nombela,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
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                                                                                                                                                                                                                                                                                                                               179
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licheninase (EC 3.2.1.73) precursor [validated] - B N;Alternate names: endo-beta-1,3-1,4-glucanase; lic C;Species: Bacilius macerans C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 lichenase Bacillus macerans

Mol. Gen. Genet. 222, 278-283, 1990
A; Title: Structure of the beta-1,3-1,4-glucanase
A; Reference number: S11927; MUID:91109712; PMID:2 Buettner, K.; Maentsaelae, Canase gene of PMID:2274030 #text_change 15-Sep-2000 Bacillus macerans: homologie

A;Status: preliminary

A;Cross-references: EMBL:X55959; R;Hahn, M.; Heinemann, U. NID: g296715; PIDN: CAA39426.1; PID:g296716

submitted to the Brookhaven Protein Data Bank, December 1994
A;Reference number: A67074; PDB:LMAC
A;Reference number: A67074; PDB:LMAC
A;Contents: annotation; X-ray crystallography, 2.3 angstroms, residues 26-37,'p',39-2
A;Note: recombinant form with residues 26-41 from Bacillus amyloliquefaciens expresse
R;Keitel, T.; Simon, O.; Borriss, R.; Heinemann, U.
Proc. Natl. Acad. Sci. U.S.A. 90, 5287-5291, 1993

RESULT 10

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A;Description: catalyzes the hydrolysis of 1,4-beta-D-glucosidic bonds in C;Superfamily: licheninase \ C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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S19012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charcone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 licheninase (EC 3.2.1.73) precursor - Bacillus polymyxa N;Alternate names: endo-beta-1,3-1,4-glucanase; lichenase C;Species: Bacillus polymyxa C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999 C;Accession: S19012 R;Gosalbes, M.J., Perez-Gonzalez, J.A.; Gonzalez, R.; Navarro, A. J. Bacteriol. 173, 7705-7710, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-25/Domain: signal sequence #status predicted <PRO> F;26-237/Product: licheninase #status experimental <MAT> F;55-84/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: EMBL:X57094; NID:g48815; PIDN:CAA40379.1;
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A; Residues: 1-238 <605>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: catalyzes the hydrolysis of 1,4-beta-D-glucosidic bonds C; Superfamily: licheninase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Contents: annotation; X-ray crystallography, 2.3 angstroms A;Note: recombinant form with residues 26-41 from Bacillus amyloliquefaciens C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Molecular and active-site structure of a Bacillus 1,3-1,4-beta-glucanase. A; Reference number: A47562; MUID:93281743; PMID:8099449
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                        Keywords: glycosidase; hydrolase; polysaccharide degradation;1-26/Domain: signal sequence #status fredicted <PRO>;27-237/Product: licheninase #status predicted <MAT>;56-85/Disulfide bonds: #status predict;d
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                         61;
                                                            -VLKHT---ATTNIPSTPGKIMMNLWNGTGVDSWLGSYNGAN-PLYAEYDWV--
                                                                                                  QEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKYYKYT 195
                                                                                                                                                                                       VDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 139
                                                                                                                                                                                                                                  SLTSPANNK-FDCGEYRSTNNYGYGLYEVSMKPAKNTGIVSSFFTYTGPSH---GTQWDE
                                                                                                                                                                                                                                                                          ALTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KHT---ATANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFLGKDTTKVQFNYYTNGVGGH----EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDI
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                                                                                                                                                                                                                                                                                                                                           Score 227.5; DB 1
Pred. No. 4.4e-09;
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Pred. No. 4e-09;
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PMID:1938968
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                                                                                                                                                                                                                                                                                                                                                                238;
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A; Gene: CAC2807
C; Superfamily:
                                                                           A; Molecule type: DNA
A; Residues: 1-246 <KUR>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                         endo-1,3(4)-beta-glucanase family 16 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: D97245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: laminarinase C;Species: Clostridium thermocellum C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-199 C;Accession: JS0611; S18726 R;Zverlov, V.V.; Laptev, D.A.; Tishkov, V.I.; Velikodvorskaja, G.A. Biochem. Biophys. Res. Commun. 181, 507-512, 1991 A;Title: Nucleotide sequence of the Clostridium thermocellum laminarinase A;Reference number: JS0611; MUID:92095946; PMID:1755832 A;Accession: JS0611
                                                                                                                                                         A; Reference number: A96900; A; Accession: D97245
                                                                                                                                                                           A; Title: Genome Sequence and Comparative Analysis of the A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                .; Daly, M.J.; Bennett, G.N.; Koonin, J. Bacteriol. 183, 4823-4838, 2001
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C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-242/Product: endo-1,3(4)-beta-glucanase #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Zverlov, V.V.; Velikodvorskaya,
Biotechnol. Lett. 12, 811-816, 19
A;Title: Cloning the Clostridium
                                          C; Genetics:
                                                           A; Experimental source:
                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                     R; Nolling, J.; Breton, G.; Omelchenko,
                                                                                                                                                                                                                                                                                                                                                         D97245
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A; Residues: 1-242 <ZVE1>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKLPL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFHTYGFEWRFDYIDFYVDGKKVYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFHTYGLEWTFNYVRWTVDGQEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQ
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    licheninase
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                                                                               GB:AE001437;
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                                                           Clostridium
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1990
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                                                                             PIDN: AAK80751.1;
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Pred. No. 7.3e-09;
                                                           acetobutylicum
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Smith, D.R.
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ster, E.W. A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A.Reference number: AB2577; PMID:11743193
A.Accession: AB3055
A.Status: preliminary
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Search completed: July 11, 2003, 10:54:14 Job time: 19 secs
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A;Residues: 1-263 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44856.1; PID:g17742502; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                        199 --EVIDETKIPQNAQKIFFSLWGTDTLKDWMGKF 230
                                                                                                                                                                                                                                                                            147 GGQVSNLT----GTQGLRFNLWSSESAA-WVGQF 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 NPGSFQSN-IITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTE 146
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1 MNIKKTAVKSALAV
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GUB_PAEMA
GUB_RHOMR
BRUIL_SOYBM
EXSH_RHIME
EXSH_RHIME
EXGR_ALTCA
E13B_BACGI
SERA_PLAFGI
SERA_PLAFGI
SERA_PLAFGI
SERA_PLAFGI
SUMA_PSEFIL
ACC8_HUMAN
GUNL_PCSEFIL
ACC8_HUMAN
GUNL_PCSEFIL
GUNA_TRIRE
SCO2_NEUCR
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Query Match 100.0%; 9 Best Local Similarity 100.0%; 1 Matches 349; Conservative 0;

Score 1824; DB 1; Pred. No. 1.9e-123;); Mismatches 0;

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Hydrolase;
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between
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BAPAL MICTOBIOL: BIOTECHNOL. 38:507-513(1993).

-I- FUNCTION: HYDROLYSES B-GLUCANS CONTAINING MIXED BETA-1,3
BETA-1,4 LINKAGES. THIS ENZYME IS THERMOSTABLE; ITS OPTI
TEMPERATURE IS NEAR 65-70 DEGREES CELSIUS.

-I- CATALYTIC ACTIVITY: Hydrolysis of 1.4-beta-D-glycosidic
in beta-D-glucans containing 1.3- and 1,4-bonds.

-I- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTR.
SIMILAR TO LICHENASE OF GERMINATING BARLEY.

-I- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                       Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
Hydrolase; Glycosidase; Signal.
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Beta-glucanase precurso
(1,3-1,4-beta-D-glucan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Louw M.E., Reid S.J., Watson T.G.; "Characterization, cloning and sequencing endo-(1,3-1,4) beta-glucanase-encoding generations."
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NCBI_TaxID=1393;
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P23904; 1AJK.
Pro; IPR000757; Glyco_hydro_16.
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MEDLINE=97124196; Pub
Yoshida K.-I., Shindo
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Tezuka H., Yuuki T., Yabuuchi S.;
"Construction of a beta-glucanase hyperproducing using the cloned beta-glucanase gene and a multi-Agric. Biol. Chem. 53:2335-2339(1989).
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(1,3-1,4-beta-D-glucan
BGLS OR BGL OR LICS OR
  MEDLINE=96178961;
Schnetz K., Stuel
                                       SEQUENCE OF 1-6 FROM STRAIN=BR151;
                                                                                            subtilis: characterization, mapping and construction deficient in lichenase, cellulase and xylanase."; microbiology 141:281-290(1995).
                                                                                                                                                        MEDLINE=95219081; PubMed=7704256;
Wolf M., Geczi A., Simon O., Borriss I
"Genes encoding xylan and beta-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          excreted
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Bacteria; Firmicutes;
NCBI_TaxID=1423;
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MCConnell D.J., Cantwell B.A.;
sequence of the gene and genetic c
B. subtilis enzyme beta-glucanase.
Acids Res. 12:5355-5367(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- - TENIPQTPQKIMMNLWPGVGVDGWTGVFDGDNTPVYSYYDWV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKDTTRIQFNYFTNGVGG----NEFYYDLGFDASESFNTYAFEWREDSITWYVNGEAVHTA
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Rel. 41, Last annotation update)
Precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
D-glucan 4-glucanohydrolase) (Lichenase).
LICS OR N15B.
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                  PubMed=8606172;
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PROTON DONOR (BY SIMILARITY).
A63C09F281FF5D13 CRC64;
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and
Krueger
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RESULT 4
GUB_BACAM
ID GUB_B
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Best Local
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PIR; A22914; LXBS.
PIR; JU0110; JU0110.
HSSP; P27051; 1GBG.
HSSP; P37051; 1GBG.
 GUB_BACAM
P07980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Purification and some properties of two enzymes from a beta Purification and some properties of two enzymes from a beta hyperproducing strain, Bacillus subtilis HL-25.";
Agric. Biol. Chem. 53:2341-2346(1989).

-i- CATALYTIC ACTIVITY: Hydrolysis of 1.4-beta-D-glycosidic in beta-D-glucans containing 1,3- and 1,4-bonds.

-i- SUBCELLULAR LOCATION: Secreted.

-i- SUBCELLULAR LOCATION: Secreted.

-i- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTR.

SIMILAR TO LICHENASE OF GERMINATING BARLEY.

-i- MISCELLANEOUS: THE SEQUENCE OF STRAIN 168 IS SHOWN.

-i- SIMILAR TO LICHENASE OF GERMINATING BARLEY.
                                                                                                                                                                                                                                                                                                                      VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Subtilist; BG10476; bg1S.
InterPro; IPR000757; d1yco_hydro_16.
Pfam; PF00722; G1yco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
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"LicT, a
the BglG
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[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X00754; CAA25328.1; -...
D00518; BAA00405.1; -...
D83026; BAA11697.1; -...
Z46862; CAA86922.1; -...
Z28340; CAA82195.1; -...
Z99124; CAB15943.1; -...
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                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                      VDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 139
                                                                                 Q-LKHTATNQIPTTPGK--IMMNLWNGTGVDEWLGSYNGVN-PLYAHYDWVRYTK 241
                                                                                                           QEVRKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                                                               ALTINVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVE
                                                                                                                                     IDIEFLGKDTTKVQFNYYTNGAG----NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDG
                                                                                                                                                                                             ALTSPAYNK-FDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPT---
                                                                                                                                                                                                                                                                                                ; Glycosidase; s
1 28
29 242
29 242
29 133
137 137
60 89
24 24
83 83
204 204
242 AA; 27268 N
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               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal;
                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                    BETA-GLUCANASE.

PYRROLIDONE CARBOXYLIC ACID.

NUCLEOPHILE (BY SIMILARITY).

PROTON DONOR (BY SIMILARITY).

BY SIMILARITY.

A -> S (IN STRAIN HL-25).

A -> L (IN STRAIN HL-25).

P -> L (IN STRAIN C120).
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                                                                                                                                                                                                                                                             Score 248;
Pred. No. 5.
               PRT;
                                                                                                                                                                                                                                                                                                       -> S (IN STRAIN HL-25).
-> S (IN STRAIN HL-25).
-> L (IN STRAIN C120).
45958DEA70F22B29 CRC64;
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              239
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RESULT 5

XYND_RUMFL

ID XYND_R

AC Q53317

DT 01-NOV

DT 01-SUN

DT 15-JUN

DE Xylana

DE Xylana

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01-AUG-1988
01-JUN-1994
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ACT_SITE
DISULFID
                        053317:
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
xylanase/beta-glucanase precursor [Includes: Endo-1,4-beta-xylanase (EC 3.2.1.8) (xylanase); Endo-beta-1,3-1,4 glucanase (EC 3.2.1.73)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
SIGNAL
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Pfam; PF00722; Glyco_hydro_16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A29091; A29091.
HSSP; P27051; 1GBG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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Bacteria; Firmicutes; Baci
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MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way that the state of the swip and the state of the swip as its content is in no way the swip as the state of the swip as th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134
                                                                                                                                                                                                                                                                                                                                                                                                                                   190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00737; GLHYDRLASE16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit institu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                   KHTATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYDWMRYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFLGKDTTKV()FNYYTNGAG---NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVIGKNPGSF()SNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26
134
57
239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 (Rel. 08,
8 (Rel. 08,
4 (Rel. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
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precursor (EC 3.2.1.73) (Endo-
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
239
134
86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-glucanohydrolase) (Lichenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOPHILE (BY SIMILARIT BY SIMILARITY:
; A76A64268A7AAAOB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BETA-GLUCANASE.
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 1.
                                                                                                                                                                                                                                                                    802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Endo-beta-1, 3-1, 4 glucanase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4e-10;
hes 75;
                                                                                                                                                                                                                                                                    ĄĄ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bу
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in no way commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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Query Match
Best Local
                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S61204; AAB26620.1; -.
HSSP; P23904; 1AJK.
InterPro; IPR003305; CBM_CenC.
InterPro; IPR003137; GH_11.
InterPro; IPR001137; GH_21.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00457; Glyco_hydro_16; 1.
Pfam; PF00722; Glyco_hydro_16; 1.
Pfam; PF02018; CBM_4_9; 1.
PRINTS; PR00911; GLHYDRLASE11.
PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucanase domains, encoded by the xynD gene of Ruminococcus flavefaciens";
J. Bacteriol. 175:2943-2951(1993).
-!- FUNCTION: CONTAINS TWO CATALYTIC DOMAINS WITH XYLANASE AND BETA-1,3-1,4 GLUCANASE ACTIVITIES.
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>: :</del>
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93259938; PubMed-8491715;
                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                           NIVMOC
                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A bifunctional enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flint H.J., Martin J., McPherson C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruminococcus flavefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linkages in xylans.

linkages in xylans.

CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in heta-D-glucans containing 1,3- and 1,4-bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in beta-D-glucans containing 1,3- and 1 PATHWAY: Xylan degradation. SIMILARITY: IN THE N-TERMINAL SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: IN THE N-TERMINAL SECTION;
G (FAMILY 11 OF GLYCOSYL HYDROLASES).
SIMILARITY: IN THE C-TERMINAL SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degradation; Hydrolase;
                                                                                                                 30
                                                                                                                                                                        Similarity
                                 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ
                                                                                             YSGGEFRTNNFYHYGYYECSMQAMKNDGVVSSFFTYTGPS---DDNPWDEIDIEILGKNT
                                                                                                                                                                                                                              546
802
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                    enzyme.
317
3244
327
5523
5523
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5524
5524
                                                                                                                                                                                                                                  89091
                                                                                                                                                                      13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McPherson C.A., Daniel A.S., Zhang J.-X.; with separate xylanase and beta(1,3-1,4)-ded by the xynD gene of Ruminococcus
                                                                                                                                                                                                                                  MW;
                                                                                                                                                      21;
EKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRA----
                                                                                                                                                Score 242.5;
Pred. No. 6e-1
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   C (BETA
                                                                                                                                                                                                                              POLY-THR.
POLY-THR.
2880A689647284AF CRC64;
                                                                                                                                                                                                                                                                                       POLY-THR
                                                                                                                                                                                                                                                                                                           NUCLEOPHILE
                                                                                                                                                                                                                                                                                                                         C (BETA-GLUCANASE).
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                              XYLANASE/BETA-GLUCANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                         (XYLANASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridiales; Lachnospiraceae;
                                                                                                                                                                    No. 6e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as its content
                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BELONGS TO FAMILY 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BELONGS
                                                                                                                                                    74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                    Indels
                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                        802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL outstation
                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENDO-
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n on
                                                                         690
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SOLUTION OF THE STREET OF THE

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HSSP; P23 InterPro;

P23904; 1AJK

IPR002105;

Dockerin_1. EF-hand.

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RESULT 6
GUB_CLOTM
EMBL; X63355; CAA44959.1; -
EMBL; X58392; CAA41281.1; -
PIR; S23498; S23498.
PIR; JS0611; JS0611.
PIR; JS0612; JS0611.
PIR; S18726; S18726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUB_CLOTM STANDARU; Fr., P29716; p37074; 01-APR-193 (Rel. 25, Created) 01-UN-1994 (Rel. 29, Last sequence update) 01-FEB-1996 (Rel. 33, Last annotation update) 01-FEB-1996 (Rel. 33, Last annotation update) Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4-1) (1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase) (Last 21,3-1,4-beta-D-glucan 4-glucanohydrolase)
                                                                                                                      entities
or send a
                                                                                                                                                                                                                                                                          Zverlov V.
Submitted
                                                                                                                                                       use by non-profit institutions as rong a modified and this statement is not removed.
                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schimming S., Schwarz W.H., Staudenbauer W. Schiucture of the Clostridium thermocellum beta-1,3-1,4-glucanase. A catalytic region lichenases joined to the reiterated domain
                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zverlov V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92095946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 27405 / DSM 1237;
MEDLINE=92155194; PubMed=1740123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LICB OR LAM1.
Clostridium thermocellum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1515;
                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                    s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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tev D.A., Tishkov V.I., Velikodvorskaja G.A.;
nce of the Clostridium thermocellum laminarinase
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                                                                             LIODeras J., Perez-Pons J.A., Querol E.;

"Molecular cloning, expression and nucleotide sequence of the endo-beta-1,3-1,4-D-glucanase gene from Bacillus licheniformis Predictive structural analyses of the encoded polypeptide.";

Eur. J. Biochem. 197:337-343(1991).
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Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL
PROSITE; PS01034; EF_HAND; UNKNOW
PROSITE; PS000448; CLOS_CELLULOSOM
                                   Querol E.;
Submitted (JUL-1991)
                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=91224124; PubMed=2026156;
                                                                                                                                                                                 Bacteria; Firmicutes;
NCBI_TaxID=1402;
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 MEDLINE=92362869;
             MUTAGENESIS
                                                              REVISIONS
                                                                                                                                                                                                          Bacillus licheniformis
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7 (Rel. 35, Las
nase precursor
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EF_HAND; UNKNOWN_2.
CLOS_CELLULOSOME_RPT;
 PubMed=1354172;
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30.9%;
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Last annotation update)
sor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
n 4-glucanohydrolase) (Lichenase).
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Pred.
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PROTON DONOR (BY SIMILARITY).

PRO/THR-RICH (LINKER).

2 X 24 AA APPROXIMATE REPEATS
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                                                                                                                                                                                                                                                                                   MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of active site carboxylic residues in Elicheniformis 1,3-1,4-beta-D-glucan 4-glucanohydrolase site-directed mutagenesis.";

J. Blol Cham Communication of the com
                                                                                                                                                                                  SEQUENCE
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PIR; S15388; S15388.
PDB; 1GBG; 07-DEC-95.
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SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
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BETA-GLUCANASES OF BACILLUS HAVE A SUBSTF
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33.7%;
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N: 85% OF WILD-TYPE ACTIVITY.
O: 33% OF WILD-TYPE ACTIVITY.
O: 50% OF WILD-TYPE ACTIVITY.
O: 50% OF WILD-TYPE ACTIVITY.
O: 0.2% OF WILD-TYPE ACTIVITY.
O: 0.2% OF WILD-TYPE ACTIVITY.
N: 0.5% OF WILD-TYPE ACTIVITY.
N: 60% OF WILD-TYPE ACTIVITY.
O: 1.5% OF WILD-TYPE ACTIVITY.
O: 1.5% OF WILD-TYPE ACTIVITY.
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N: 60% OF WILD-TYPE ACTIVITY.
N: 70% OF WILD-TYPE ACTIVITY.
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N: NO CHANGE IN ACTIVITY.
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3.6.1e-10; 77;
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RESULT 8

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DE HYPOTHRETCA.
GN YGR189C OR (OS Saccharomyc)
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RA Nombela C.;

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01-NOV-1997 (Rel. 3
Hypothetical 52.8)
YGR189C OR G7553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Saccharomycetales;
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Pfam; PF00722; Glyco_hydro_16; 1.
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Arroyo J., Garcia-Gonzalez M., Garcia-Saez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288c;
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an email.to license@isb-sib.ch).
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                           AGGETNYNDAPFTMYIEKVIVTDYSTGKKYTYGDQSGSW-ESIEADGGSIYGRYDQAQE-
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Hahn M., Keitel T., Heinemann U.; "Crystal and molecular structure at 0.16-nm resolution Bacillus endo-1,3-1,4-beta-D-glucan 4-glucanohydrolase Eur. J. Biochem. 232:849-858(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93094208; PubMed-1360982; Hoej P.B., Condron R., Traeger J.C., McA: "Identification of glutamic acid 105 at amyloliquefactens 1,3-1,4-beta-D-glucan epoxide-based inhibitors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91109712; PubMed-2274030; Boorriss R., Buettner K., Maentsaelae P.; "Structure of the beta-1,3-1,4-glucanase homologies to other beta-glucanases."; Mol. Gen. Genet. 222:278-283(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS). MEDLINE-96028129; PubMed-7588726;
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Paenibacillus macerans (Bacillus macerans).
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
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01-JUN-1994 (Rel. 29,
15-JUL-1998 (Rel. 36,
                                                                                                                                 entities requires a license agreement (
or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic in beta-D-glucans containing 1,3- and 1,4-bota-MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTR SIMILAR TO LICHENASE OF GERMINATING BARLEY.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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S11927; S
2AYH; 31-
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                                                                                                                                                                 non-profit institutions as long and this statement is not removed.
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precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
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27-FEB-95
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Last sequence update)
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY)
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p3363;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sec
15-JUN-2002 (Rel. 41, Last an
Endo-1,3-1,4-beta-glycanase e)
biosynthesis protein exoK).
EXOK_OR_RB1080 OR_KBB20955.
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"Two beta-glycanase genes are clustered in Bacillus polymyxa:
molecular cloning, expression, and sequence analysis of genes
encoding a xylanase and an endo-beta-(1,3)-(1,4)-glucanase.";
J. Backeriol. 173:7705-7710(1991).
-i- CAPALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages
in beta-D-glucans containing 1,3- and 1,4-bonds.
-i- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGE
SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-i- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
            Rhizobium meliloti (Sinorhizobium meliloti). Plasmid pSymB (megaplasmid 2).
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Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL HYDROI F11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes; F
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PR00737; GLHYDRLASE16;
PS01034; GLYCOSYL_HYDROL_F16;
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and this statement
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Pred. No. 1.6e-09;
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
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Proteobacteria;

alpha subdivision; Rhizobiaceae group;

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SOT TO THE PROPERTY OF THE PRO
                            Query Match
Best Local
     Matches
                                                                                                                                                                                                          InterPro; ir Novo---
Pfam; pF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                 EMBL; L20758; AAA16048.1; -.
EMBL; Z17219; CAA78927.1; -.
EMBL; AL603645; CAC49480.1; -.
HSSP; P23904; 1AJK.
InterPro; IPR000757; Clyco_hydro_16.
                                                                                                  CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            depolymerize nascent succinglycan chains.";
Proc. Natl. Acad. Sci. U.S.A. 95:4912-4917(1998).
-I- FUNCTION: CLEAVES HIGH MOLECULAR WEIGHT SUCCINGGLYCAN TO YIELD LAW SUCCINGLYCAN. DYNAMICALLY REGULATE THE MOLECULAR WEIGHT DISTRIBUTION OF SUCCINGGLYCAN BY CLEAVING NASCENT SUCCINGGLYCAN ONLY DURING A LIMITED PERIOD AFTER ITS SYNTHESIS, PERHAPS BEFORE IT UNDERGOES A TIME-DEPENDENT CHANGE IN ITS CONFORMATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Becker A., Kleickmann A., Arnold W., Puehler A.; "Analysis of the Rhizobium meliloti exoH/exoK/exoL fragment: shows homology to excreted endo-beta-1,3-1,4-glucanases and resembles membrane proteins"; mol. Gen. Genet. 238:145-154(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucksmann M.A., Reuber T.L., Walker G.C.;
"Family of glycosyl transferases needed for succinoglycan by Rhizobium meliloti.";
J. Bacteriol. 175:7033-7044(1993).
                                                                                                                                                                                                  Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
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Finan T.M., Weidner S., Wong K., Buhrmester
Vorhoelter F.J., Hernandez-Lucas I., Becker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-RCR2011 / SU47;
MEDLINE-93241147; PubMed-8479421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete sequence of the 1,683-kb pSymB meg. fixing endosymbiont Sinorhizobium mellioti."; Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Golding B., Puehler A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21396508;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 York G.M., Walker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobiaceae; S
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Exopolysaccharide biosynthesis. SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G.M., Walker G.C.;
Rhizoblum mellloti ExoK and ExsH glycanases specifically
Rhizoblum mellloti ExoK and ExsH glycanases specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
                            Similarity
                                                                                                                                                                                                    proteome.
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93
269
     Conservative
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30083 ,
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                    10.8%;
                                                                                                  X
X
  31;
                    Score 197;
Pred. No. 2.
                                                                                             ENDO-1,3-1,4-BETA-GLYCANASE
ACGEIQTRKR -> LRRNPDAQG (IN
073CC7ED65EF2611 CRC64;
  Mismatches
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lot1.";
                       DB 1;
.8e-07
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RESULT 12
UTR2_YEAST
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Arau Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cher Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S. Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smi Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

    Pfam; PF00722; Glyco_hydro_16;

    DOMAIN
    234
    322

    DOMAIN
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    CONFLICT
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    CONFLICT
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                                                                                                                           EMBL; U18779; AAB65002.1; ALT_INIT. EMBL; L22173; AAA34941.1; -. EMBL; S65964; AAD13975.1; -. EMBL; S66130; AAB28444.1; -. EMBL; S30839; S30839.
                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
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SEQUENCE FROM N.A.
Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., R
Mei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
Charlet G. (FEB-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=B-6441;
MEDLINE=94016558;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UTR2 protein (Unknown transcript 2 UTR2 OR YEL040W OR SYGP-ORF18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27,
01-OCT-1994 (Rel. 30,
01-OCT-1996 (Rel. 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UTR2_YEAST P32623;
                                                                             HSSP; P23904; 1AJO.
SGD; S0000766; UTR2.
InterPro; IPR000757; Glyco.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                           "The gene clusters ARC and COR on chromosomes 5 and of Saccharomyces cerevisiae share a common ancestry. J. Mol. Biol. 233:372-388(1993).
                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: SOME, TO YEAST YGR189C
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Last sequence
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Best Local
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                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-93005704; PubMed-1840916;
Medford J.I., Elmer J.S., Klee H.J.;
Medford J.T. and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
SEQUENCE
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
MERI-5 protein precursor (Endo-xyloglucan transendo-1,4-beta-D-glucanase).
MERI-5 OR MERI5B OR SEN4 OR AT4G30270 OR F9N1:
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckae Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtl
                                                   SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
Mayer K.F.X., Schueller C., Wambut
                                                                                                                                                                                                STRAIN-cv. Columbia;
Kamimai T., Tomita E
Submitted (JUL-1995)
                                                                                                                                                                                                                                                                  apical meristems.";
Plant Cell 3:359-370(1991).
                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons; eurosids II; Brassicales; Brassicaceae; Arabi
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                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress
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(AUG-1995)
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Pred. No. 1.3e
49; Mismatches
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EMBL/GenBank/DDBJ databases.
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No. 1.3e-06;
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RA Cheffor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Trancs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
Ra Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Zaccaria P., Bedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Zaccaria P., Bedhia N., Gnoj L., Schutz K., Habermann K.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Abu-Threideh J.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Schneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Schoneking T., Kalicki J., Graves T., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Man J., Shong J., Preston R., Vilone M., Johnson A.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Man J., Konjonessy A., Rodriguez M., Hoffman J., Till S.,
RChen E., Marra M., Martlenssen R., McCombie W.R.,
Rodriguez M., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martlenssen R., McCombie W.R.,
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Vos P., H
                                                                                                                                                                                                                                                                                               senescence induced by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv.
Raynal M.,
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Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R.,
                                                                                                                                                                                                                                                   Plant Mol. Biol 37:445-454(1998)
                                                                                                                                                                                                                                                                      Arabidopsis.",
                                                                                                                                                                                                                                                                                                  WEDLINE-98.778374; FubMed=9617812;
WEDLINE-98.778374; FubMed=9617812;
Park J.-H., Oh S.A., Kim Y.H., Woo H.R., Nam H.G.;
Park J.-H., Oh S.A., Kim Y.H., Woo H.R., Nam H.G.;
Park J.-H., Oh S.A., Kim Y.H., Woo H.R., Nam H.G.;
Park J.-H., Oh S.A., Kim Y.H., Woo H.R., Nam H.G.;
Park J.-H., Oh S.A., Kim Y.H., Woo H.R., Nam H.G.;
Park J.-H., Oh S.A., Kim Y.H., Woo H.R., Nam H.G.;
Park J.-H., Oh S.A., Kim Y.H., Woo H.R., Nam H.G.;
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                                                                                                                                                              FOUND IN SEEDLINGS AND MERISTEMS.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
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COlumbia; TISSUE-Green siliques;

Grellet F., Laudie M., Meyer Y., Cooke R., De
-----1092) to the EMBL/GenBank/DDBJ databases.
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isel J., Zimmerı
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                                                                                                                 .1 sequence differs from that 158; 178; 183; 189; 190; 194
                                                                    sequence of and 104.
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Matches 56
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EMBL; D63508; BAA09783.1; -.
EMBL; AL109796; CAB52471.1; -.
EMBL; AL109796; CAB51020.1; -.
EMBL; AV0351.56; AAK59660.1; -.
EMBL; AV0351.56; AAK59600.1; -.
EMBL; AV035027; AAL34201.1; -.
EMBL; Z17602; CAA79012.1; ALT_FRAME.
EMBL; Z17602; CAA79012.1; ALT_FRAME.
EMBL; AF035384; AAC39467.1; -.
PIR; J01022; J01022.
PIR; J01022; J01022.
HSSP: P23904; LAJK.
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CONFLICT
SEQUENCE
                                                                                                                          Spilliaert R., Hreggvidsson G.O., Kristjan
Eggertsson G., Palsdottir A.;
"Cloning and sequencing of a Rhodothermus
for a thermostable beta-glucanase and its
                                                                                                                                                                                                                                                     STRAIN=21 / ITI-378;
MEDLINE=95010084; PubMed=7925416;
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=29549;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Bacteroidetes; Sphi
Crenotrichaceae; Rhodothermus
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PF00722; Glyco_hydro_16; 1.
PF: PS01034; GLYCOSYL_HYDROL_F16;
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A -> G (IN REF. 1).
648F042BC7ADED86 CRC64;
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Ol-JUN-1994 (Rel. 29, Last
15-JUN-2002 (Rel. 41, Last
Brassinosteroid-regulated p
Glycine max (Soybean).
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P35694;
01-JUN-1994
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MEDLINE-9419788; PubMed-8115544;
Zurek D.M., Clouse S.D.;
"Molecular cloning and characterization of a b"Molecular cloning and characterization ax L.)
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                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Str
Spermatophyta; Magnoliophyta;
eurosids I; Fabales; Fabaceae
           the
                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                  gene from elongating soybean (Glycine max L.) epicotyls.";
Plant Physiol. 104:161-170(1994).
-i- FUNCTION: POSSIBLE ROLE IN BRASSINOSTEROID-STIMULATED EL
-i- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
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Pfam; PF00722; Glyco_hydro_16; 1.
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CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
              European Bioinformatics Institute.
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PROTON DONOR (BY SIMILARITY).
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HSSP; P23904: 1AJK.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE: PS01034; GLYCOSYL_HYDROL_F16; 1.
Glycosidase: Hydrolase: Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                  156 KPQHIIFLVDNTPIRVFKNAEPLGVPFPKNQPMRIYSSLWNADDWATRGGLVKTDWSKAP 215
                                                                                                                                                                    129 TPNYVRWTVDGQEVRKTEGGQVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKLP 181
                                                                 216 FTAYYRNFKAIEFS 229
                                                                                                   182 LFQFINWVKVYKYT 195
                                                                                                                                                                                                                                                                          99 SQGPTHDEIDFEFLGNLSGDPYILHTNIFTQGKG-NREQQFYLWFDPTRN--FHTYSIIW 155
                                                                                                                                                                                                                             72 ADGRPWVEVDIEVLGK---NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEW 128 : | | : | | | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                  1 30 POTENTIAL.
31 283 BRASSINOSTEROID-REGULATED PROTEIN BRU1.
283 AA; 32254 MW; C248810EC7835737 CRC64;
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Query Match
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Matches 247; Conserv

99.6%; Score 1328; DB 1; nilarity 100.0%; Pred. No. 1.2e-103; Conservative 0; Mismatches 0;

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PROSITE; PS01034; GLYCOSYL_HYDROL_F:
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Louw M.E., Reid S.J., Watson T.G.;
"Characterization, cloning and sequencing
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European Bioinformatics Institute. There a
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BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
A63C09F281FF5D13 CRC64;
                                                                             POTENTIAL
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Best Local S
Matches 63
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13-AUG-1987 (Rel. (
01-NOV-1995 (Rel. )
15-JUN-2002 (Rel. )
                                                                                                                                                                                                          Miwa Y., Fujita Y.;

"Sequencing of a 65 kb region of containing the lic and cel loci, covering the gnt-sacXY region.";

Microbiology 142:3113-3123(1996).
                                                                                                    MEDLINE-95219081; PubMed=7704256; Wolf M., Geczi A., Simon O., Borriss R.; "Genes encoding xylan and befarglucan hydrolysing subtilis: characterization, mapping and constructideficient in lichenase, cellulase and xylanase."; Microbiology 141:281-290(1995).
                                                                                                                                                                                                                                                                                                                      Agric.
           the
                                                        STRAIN-BR151;
MEDLINE-96178961;
                                                                                                                                                                                                                                                                      MEDLINE=97124196; PubMed=8969509; Yoshida K.-I., Shindo K., Sano H.,
                                                                                                                                                                                                                                                                                                                                Tezuka H., Yuuki T., Yabuuchi S.; "Construction of a beta-glucanase hyperproducing Bacillus subtilis using the cloned beta-glucanase gene and a multi-copy plasmid."; Agric. Biol. Chem. 53:2335-2339(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                Murphy N., McConnell D.J., Cantwell B.A.;
"The DNA sequence of the gene and genetic control excreted B. subtilis enzyme beta-glucanase.";
Nucleic Acids Res. 12:5355-5367(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
Bacteria; Firmicutes;
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                       "LicT,
                                            Schnetz K.,
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         Bacillus family.";
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precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
D-glucan 4-glucanohydrolase) (Lichenase).
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                      subtilis
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EMBL; D00518; BAA00405.1; -.
EMBL; D00518; BAA11697.1; -.
EMBL; D46862; CAA86922.1; -.
EMBL; Z4862; CAA86922.1; -.
EMBL; Z28340; CAA82195.1; -.
EMBL; Z99124; CAB15943.1; -.
PIR; A22914; LXBS.
PIR; J00110; J00110.
HSSP; P27051; 1GBG.
Subtilist; BG10476; bg1S.
Interpro; IPR000757; Glyco_hydro_16; 1.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                     Q53317;
01-NOV-1997
01-NOV-1997
15-JUN-2002
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Purification and some properties of two enzymes from a beta hyperproducing strain, Bacillus subtilis HL-25.";

Agric. Biol. Chem. 53:2341-2346(1989).

- CAPALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic in beta-D-glucans containing 1,3- and 1,4-bonds.

- SUBCELLOUAR LOCATION: Secreted.

- MISCELLANEOUS: BETA-GLUCANASES OF BACILUS HAVE A SUBSTR SIMILAR TO LICHENASE OF GERMINATING BARLEY.

- MISCELLANEOUS: THE SEQUENCE OF STRAIN 168 IS SHOWN.

- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
Xylanase/beta-glucanase
                                                                                                                    XYND_RUMFL
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                                                                                                                                                                                                                                                                                                                           TKVQFNYYTNGAG----NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHTATNQ
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27268 MW;
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precursor [Includes: Endo-1,4-beta-xylanase
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Pred. No. 1.4e-13;
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A -> S (IN STRAIN HL-25).
P -> L (IN STRAIN C120).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANGE
                                                                                                                                                                                                                                                                                                                           199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
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Дb
                        δÃ
                                                                                                     Query Match
Best Local S
Matches 58
                                                                                                             DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 175:2943-2951(1993).

1- FUNCTION: CONTAINS TWO CATALYTIC DOMAINS WITH XYLANASE AND ENDOBERA-1, 3-1,4 ELUCANASE ACTIVITIES.

1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.

1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.

1- PARHWAY: Xylan degradation.

1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO FAMILY 16 OF CITYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A bifunctional enzyme, with separate xylanase and beta(1,3-1,4)-glucanase domains, encoded by the xynD gene of Ruminococcus flavefaciens.";
J. Pacteriol
                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                        PRINTS: PRO0911; GLHYDRLASE11.

PRINTS: PRO0737; GLHYDRUASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00457; Glyco_hydro_11; Pfam; PF00722; Glyco_hydro_16; Pfam; PF02018; CBM_4_9; 1.
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003305; CBM_CenC.
InterPro; IPR001137; GH_11.
InterPro; IPR000757; Glyco_hydro_16.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S61204; AAB26520.1; -. HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruminococcus
                                                                                                                                                                                                                                                                  Multifunctional
                                                                                                                                                                                                                                                                              Xylan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XYND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
  634
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                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.2.1.8) (Xylanase); Endo-beta-1,3-1,4
3-1,4-beta-D-glucan 4-glucanohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLYCOSYL HYDROLASES.
YSGGEFRTNNFYHYGYYECSMQAMKNDGVVSSFFTYTGPS---DDNPWDEIDIEILGKNT
                        FSGAELYTLEEVQYCKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                degradation;
                                                   1 Similarity
58; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Firmicutes;
                                                                                                  245
524
556
124
124
226
684
532
532
802
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               flavefaciens.
rmicutes; Clostridia; Clostridiales; Lachnospiraceae;
                                                                                                   ΑA;
                                                                                                                                                                                                                                                                 enzyme
                                                                                                              802
244
523
523
525
802
124
226
684
529
553
                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                   89091
                                                             18.2%;
                                                                                                   WW.
                                       Pred. No. 1e-12;
1; Mismatches 74;
                                                                                                                          PROTON DONOR (BY SIMILARITY) NUCLEOPHILE (BY SIMILARITY). POLY-THR. POLY-THR.
                                                                                                               POLY-THR
                                                                                                                                                                          C (BETA-GLUCANASE).
NUCLEOPHILE (BY SIM
                                                                                                                                                                                                                           XYLANASE/BETA-GLUCANASE A (XYLANASE).
                                                                                                                                                                                                      LINKER.
                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                              Glycosidase;
                                                                                                   2880A689647284AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce,
                                                                                                                                                                            (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucanase (EC 3.2.1.73)
(Lichenase)].
                                                                                                                                                                                                                                                                              Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                   CRC64;
                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELLULASE FAMILY
                                                                          802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
                                                   13;
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                                                 Gaps
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GUB_BACAM
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                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUB_BACAM
P07980;
01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hofemeister J., Kurtz A., Borriss R., Knowles J.;
"The beta-glucanase gene from Bacillus amyloliquefaciens shows
extensive homology with that of Bacillus subtills.";
Gene 49:177-187(1986).
-I- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages
-I- CATALYTIC ACTIVITY: Hydrolysis of 1,4-bonds.
-I- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGE
SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-I- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel.
01-AUG-1988 (Rel.
01-JUN-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A29091; A29091.
HSSP; P27051; 1GBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M15674; AAA87323.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus amyloliquefaciens.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BE 20/78;
  193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87192007; PubMed-3106158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1390
                                                      123
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                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                         SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
ATTQIPAAPGK - - IMMNLWNGTGVDDWLGSYNGVN - PIYAHYDWMRYRK
                                                EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
                                                                                                                                                     GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                           SYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDIEFL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQDIPKTPGKIMMNAWPGLTVDDWLKAFN-GRTPLTAHYQWVTYNK
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                                                                                                    GKDTTKVQFNYYTNGAG----NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TQVQFNYYTNGQGKH----EKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRA----
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000757; Glyco_hydro_16
                                                                                                                                                                                                                                                                                                                                                                                                                    26
134
57
239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycosidase;
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08, Created)
08, Last sequence 29, Last annotations 20, Last annotations
                                                                                                                                                                                                                                                                                                                                                                                                                                                    239
134
86
                                                                                                                                                                                                                                                                                                                                             17.98;
34.38;
                                                                                                                                                                                                                                                                                                                                                                                                                         26928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
                                                                                                                                                                                                                                                                                                                                          Score 238.5;
Pred. No. 5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                            BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      A76A64268A7AAA0B CRC64;
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239
                                                                                                                                                                                                                                                                                                               .4e-13;
les 74;
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                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration -
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
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RESULT 6
GUB_CLOTM
                                                                                                                                                                                                                    PIR;
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p29716; p37074;
01-APR-1993 (Rel. 25, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
[1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase) (Laminarinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning the Clostridium thermocellum thermostable laminarinase ger in Escherichia coli; the properties of the enzyme thus produced."; Biotechnol Lett. 12:811-816(1990).

1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkage in beta-D-glucans containing 1.3- and 1,4-bonds.

1- SUBUNIT: MAY FORM PART OF A MULTIENZYME COMPLEX (CELLULOSOME).

1- DOMAIN: A 24 RESIDUES DOMAIN IS REPEATED TWICE IN THIS ENZYME I. DOMAIN: A 24 RESIDUES DOMAIN GELLUM CELLULOSOME ENZYMES. THIS DOMAIN MAY FUNCTION AS THE BINDING LIGAND FOR THE SIL COMPONENT.

MELL AS IN OTHER C. THERMOCELLUM CELLULOSOME ENZYMES. THIS DOMAIN MAY FUNCTION AS THE BINDING LIGAND FOR THE SIL COMPONENT.

1- SIMILARITY: BELLONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
InterPro; IPR002048; EF-hand.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00404; Dockerin_1; 2.
Pfam; PF007722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                         EMBL; X63355; CAA44959.1; EMBL; X58392; CAA41281.1;
                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-F7
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MEDLINE=92155194; PubMed=1740123;
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k; JS0611; JS0611.
k; S18726; S18726.
kp; P23904; 1AJK.
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                                                                                                                     Lloberas J., Perez-Pons J.A., Querol E.;
"Molecular cloning, expression and nucleotide sequence of the
endo-beta-1,3-1,4-D-glucanase gene from Bacillus licheniformis
Predictive structural analyses of the encoded polypeptide.";
Eur. J. Biochem. 197:337-343(1991).
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REPEAT
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01-NOV-1997 (Rel. 35, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                    Planas A., Juncosa M., Lloberas J., "Essential catalytic role of Glul34
                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=91224124; PubMed=2026156;
                                                                                                                                                                                                                                                                                                                               GUB_BACLI
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          glucanohydrolase
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MEDLINE=92362869; PubMed=1354172;
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2 X 24 AA APPROXIMATE REPEATS
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Pfam; PF00722; Glyco_hydro_16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucanohydrolase at 1.8-A resolution."; FEBS Lett. 374:221-224(1995).
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J. Biol. Chem. 269:14530-14535(1994).
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Juncosa M., Pons J., Dot T., Operol E., Planas A.;
"Identification of active site carboxylic residues in Elicheniformis 1,3-1,4-beta-D-glucan 4-glucanohydrolase
                                                                                                                                                                                                                                                                                     SEQUENCE
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"Crystal structure of Bacillus licheniformis 1,3-1,4-beta-D-glucan
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MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
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EGGQVSNLTGTQGLRENLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
                                                           GKDTTKVQFNYYTNGVG----NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-LKHT
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                                                                                                                                                           SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s requires a license agreement (See http://www.isb-sib.ch/announce/an email tc license@isb-sib.ch).
                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308:141-145(1992)
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33.7%;
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Pred. No. 3.1e
25; Mismatches
                                                                                                                                                                                                                                                                                 D->N: NO CHANGE IN 651188D9AAD609A5
                                                                                                                                                                                                                                                                                                                           BETA-GLUCANASE
NUCLEOPHILE.
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                                                                                                                                                                                                                                                                                                                     N: 30% OF WILD-TYPE ACTIVITY.
N: 85% OF WILD-TYPE ACTIVITY.
O: 35% OF WILD-TYPE ACTIVITY.
O: 50% OF WILD-TYPE ACTIVITY.
O: 50% OF WILD-TYPE ACTIVITY.
N: 15% OF WILD-TYPE ACTIVITY.
N: 0.5% OF WILD-TYPE ACTIVITY.
O: 0.5% OF WILD-TYPE ACTIVITY.
O: COMPLETE LOSS OF ACTIVITY.
O: COMPLETE LOSS OF ACTIVITY.
N: 65% OF WILD-TYPE ACTIVITY.
N: 60% OF WILD-TYPE ACTIVITY.
N: 60% OF WILD-TYPE ACTIVITY.
N: 80% OF WILD-TYPE ACTIVITY.
N: 70% OF WILD-TYPE ACTIVITY.
                                                                                                                                                                                                                            229.5;
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                                                                                                                                                                                                                              .le-12;
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ATTQIPQTPGK--IMMNLWNGAGVDEWLGSYN-GVTPLSRSLHWVRYTK

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01-NOV-1991
01-JUN-1994
15-JUL-1998
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P23904;
             PDB; 1AJO
InterPro;
                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                 EMBL;
PIR; ;
                                                                                                                                                                                                                                                                                          EUR. J. Biochem. 232:849-858(1995).

-i- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic link in beta-D-glucans containing 1,3- and 1,4-bonds.

-i- MISCELLANEOUS: BETA-CLUCANNSES OF BACILLUS HAVE A SUBSTRATE SIMILAR TO LICHENASE OF GERMINATING BARLEY.

-i- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93094208; PubMed=1360982; Hoej P.B., Condron R., Traeger J.C., McA "Identification of glutamic acid 105 at amyloliquefactens 1,3-1,4-beta-D-glucan epoxide-based inhibitors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
Paenibacillus macerans (Bacillus macerans).
Bacteria: Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93281743; PubMed-8099449;
Keitel T., Simon O., Borriss R., Heinemann
"Molecular and active-site structure of a E
                                                                                                                                                                                                                                                                                                                                                                              "Crystal and molecular structure at 0.16-nm resolution Bacillus endo-1,3-1,4-beta-0-glucan 4-glucanohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96028129; PubMed-7588726; Hahn M., Keitel T., Heinemann U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **Borriss R., Buettner K., Maentsaelae P.; 

"Structure of the beta-1,3-1,4-glucanase homologies to other beta-glucanases."; 

Mol. Gen. Genet. 222:278-283(1990).
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MEDLINE=91109712; PubMed=2274030;
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                            1CPM;
1CPN;
1MAC;
1AJK;
1AJO;
                                                                                                                                               x55959;
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                           77: S11927.
31-MAR-95.
31-OCT-93.
22-JUN-94.
22-JUN-94.
27-FEB-95.
06-MAY-98.
             IPR000757; Glyco_hydro_16
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Glyco_hydro_16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McAuliffe J.C., Stone at the active site of
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Bacillus
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Matches 59
                                        GUB_PAEPO STAN
P45797;
01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
15-JUL-1998 (Rel. 3
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ACT_SITE
ACT_SITE
                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
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Paenibacillus polymyxa
Bacteria; Firmicutes; F
NCBI_TaxID=1406;
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SIGNAL
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                                                                                                                                                                                                                     SEQUENCE
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                                                                                                       TANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT
                                                                                                                                          GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ
                                                                                                                                                             FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQMDEIDIEFLGKDT
                                                                                                                    VSNLTGTQG-LRENLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT
                                                                                                                                  TKVQFNYYTNGVGGH----EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VLKHT----A
                                                                                                                                                                           FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP
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; GLYCOSYL_HYDROL_F16;
sidase; Signal; 3D-str
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191
209
216
236
236
26589 MW;
                                                                                                                                                                                                                                                                     17.0%;
        Bacillales;
      (Bacillus polymyxa).
Bacillales; Paenibacillaceae;
                                                                                                                                                                                          23;
                                                                                                                                                                                        Score 226; DB Pred. No. 5.9e 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA-GLUCANASE.
NUCLEOPHILE (BY :
PROTON DONOR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       E->D, N, A, L, P, R, H, C, S, Y: LOSS OF ACTIVITY.
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                                                                                                                                                                                                                     436EABCDFFC87781 CRC64;
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                                                                                                                                                                                               226;
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5.9e-12;
1es 70;
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Y SIMILARITY).
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                                  glucanase)
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EXOK_RHIME
ID EXOS,
AC P33693
AC P33693
DT 01-FEB
DT 15-JUN
DE Endo-11
DE biosyn
GN EXOK O
OS Rhizob
OG Plasmi
OC Bacter
OC Rhizob
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RN [1]
RP SEQUEN
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Best Local :
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                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endo-1,3-1,4-beta-glycanase exoK precursor (EV)
biosynthesis protein exoK).
EXOK OR RB1080 OR SMB20955.
Rhizobium meliloti (Sinorhizobium meliloti).
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ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gosalbes M.J., Perez-Gonzalez J.A., Gonzalez R., Navarro A.;
"Two beta-glycanase genes are clustered in Bacillus polymyxa:
molecular cloning, expression, and sequence analysis of genes
encoding a xylanase and an endo-beta-(1,3)-(1,4)-glucanase.";
J. Bacteriol. 173:7705-7710(1991).
-i- CAPALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages
in beta-D-glucans containing 1,3- and 1,4-bonds.
-i- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGE
SIMILAR TO LICHENASE OF GERMINATING BARLEY.
                                                                                                                                                                                                                                        EXOK_RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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   MEDLINE=94042869; PubMed=8226645;
                 STRAIN-1021
                             SEQUENCE FROM N.A
                                                                                                      Plasmid pSymB (megaplasmid 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
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Pfam; PF00722; Glyco_hydro_16; 1.
                                                                                         Bactería;
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SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                127
                                                                                                                                                                                                                                                                                                                  193
                                                                                                                                                                                                                                                                                                                                                                          140 TKVQFNYYTNGVGGH---EKIINLGFDASTSFHTYAFDWQPGYIKWYVDG-VLKHT---A 192
                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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                                                                                                                                                                                                                                                                                                                                              VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                                                                                                                                                                                                                                                                                                                              GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                  TTNIPSTPGKIMMNLWNGTGVDSWLGSYNGAN-PLYAEYDWV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and this statement is not removed
                                                                        Proteobacteria; alpha subdivision; Rhizobiaceae group;
sae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 225; DB 1;
Pred. No. 7.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOPHILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA-GLUCANASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C0CF7B4EA5D40E8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                          269
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                                                                                                                                                               (EC
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                                                                                                                                                              3.2.1.-) (Succinoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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В
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                                                                                                                                                                                       Matches
                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The Rhizobium meliloti ExoK and ExsH glycanases specifically depolymerize nascent succinoglycan chains."

Proc. Natl. Acad. Sci. U.S.A. 95:4912-4917(1998).

-1- FUNCTION: CLEAVES HIGH MOLECULAR WEIGHT SUCCINOGLYCAN TO YIELD LMW SUCCINOGLYCAN. DYNAMICALLY REGULATE THE MOLECULAR WEIGHT DISTRIBUTION OF SUCCINOGLYCAN BY CLEAVING NASCENT SUCCINOGLYCAN ONLY DURING A LIMITED PERIOD AFTER ITS SYNTHESIS, PERHAPS BEFORE IT UNDERGOES A TIME-DEPENDENT CHANGE IN ITS CONFORMATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-RCR2011 / SU47;
STRAIN-RCR2011 / SU47;
MEDLINE=93241147; PubMed=8479421;
Becker A., Kleickmann A., Arnold W., Puehler A.;
"Analysis of the Rhizobium meliloti exoH/exoK/exoL fragment:
shows homology to excreted endo-beta-1,3-1,4-glucanases and E
resembles membrane proteins.";
Mol. Gen. Genet. 238:145-154(1993).
                                                                                                                          SEQUENCE
                                                                                                                                                        CHAIN
                                                                                                                                                                                                PROSITE: PS01034; GLYCOSYL_HYDROL_F16; 1.
Exopolysaccharide synthesis; Glycosidase; Hydrolase; Signal; Plasmid;
                                                                                                                                                                                                                                                                                              EMBL; Z17219; CAA78927.1; -. EMBL; AL603645; CAC49480.1;
                                                                                                                                                                                                                                                                                                            EMBL; L20758; AAA16048.1; -. EMBL; Z17219; CAA78927.1; -.
                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION. MEDLINE=98226741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finan T.M., Weid
Vorhoelter F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Family of glycosyl transferases needed succinoglycan by Rhizobium meliloti."; J. Bacteriol. 175:7033-7044(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucksmann M.A., Reuber T.L., Walker G.C
                                                                                                                                          CONFLICT
                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                               Pfam; PF00722; Glyco_hydro_16; PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete sequence of the 1,683-kb pSymB megaplasmid fixing endosymbiont Sinorhizobium meliloti."; Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Golding B., Puehler
                                                                                                                                                                                                                                                                 InterPro; IPR000757; Glyco_hydro_16.
                                                                                                                                                                                                                                                                                 HSSP; P23904;
                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21396508; PubMed=11481431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fork G.M.,
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   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Exopolysaccharide biosynthesis.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGREGATION STATE.
                                                                                                                                                                                       Lete
 VKERNFACGEIQTRKRFGYGTYEARIKAADGSGLNSAFFTYIGP--
                              VSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEV
                                                                             Similarity
                                                                                                                                                                                   proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Walker G.C
                                                                                                                          269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weidner S., Wong K., Buhi
F.J., Hernandez-Lucas I.,
                                                             Conservative
                                                                                                                                                                                                                                                                                  1AJK
                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9560202;
                                                                                                                          30083 MW;
                                                                             14.8%;
32.5%;
                                                             31;
                                                                             Score 197; 1
                                                                                                                      ENDO-1,3-1,4-BETA-GLYCANASE
ACGEIQTRKR -> LRRNPDAQG (IN
O73CC7ED65EF2611 CRC64;
                                                                                                                                                                     POTENTIAL
                                                             Mismatches
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                                                   DB 1,
1.8e-09;
61;
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Cowie
                                                                                        Length 269;
                                                             Indels
 -ADKKPHDEIDFEV
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                                                             12;
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                                                           Gaps
143
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LGKNPGSFQSN-IITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVR

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 52.8 kDa protein in BUB1-HIP1 intergenic region.
7GR189C OR 67553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YG46_YEAST
P53301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z72974; CAA97215.1; -. EMBL; X99074; CAA67525.1; -. HSSP; P23904; IAJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The second of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm of Saccharomyces cerevisiae chromosome VII."; Yeast 13:357-363(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00722; Glyco_hydro_16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arroyo J., Garcia-Gonzalez M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD; S0003421; CRH1.
InterPro; IPR000757; Glyco_hydro_16.
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                                                                                                                                                                                                      139
                                                                                                    198
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252 VIVTDYSTGKKYTYGDQSGSW-ESIEADGGSIYGRYD
                                                  166 VKVYKYTPGQGEGGSDFTLDWTDNFDTFDGSRWGKGD
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                                                                                                                                                                                                                                                                                                                                                        MVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIE 60
                                                                                                                                                                                                      WVGGDNTQFQSNFFSKGDTTTYDRGEFHGVDTPTDK-FHNYTLDWAMDKTTWYLDGESVR
                                                                                                                                                                                                                                                                                                        MTLAKRYDNPSLKSNFYIMYGKLEVILKAANGTGIVSSFYLQSDDLD-----EIDIE 138
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                                                                                                                                              KTEGGQVSNLTGTQG-----
                                                                                                                                                                                                                                                   VLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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-Gonzalez M., Garcia-Saez M.I.,
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357
391
                                                                                                                                                                                                                                                                                                                                                                                                                                  13.7%;
26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 182.5; DB 1; Length 507; Pred. No. 6.1e-08;
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POLY-SER.
POLY-SER.
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  287
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RESULT 12
MER5_ARATH
              RA Reichert B., Portetelle D., Perez Alonso M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Holzer S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Pettett A., Rajandream M.A., Cronin A., Quall M., McLay K., Mayes R.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Gabel C., Fuchs M., Fartmann B., Granderah K., Dauner D., Herzl A.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Gibbons T., Weber N., Berger C., Monfort A., Casacuberta E.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Frishman D., Berler C., Scholter P., Heber S., Francs P., Bielke C.,
RA Frishman D., Berder C., Schott K., Johnson S.,
RA Kerlicki J., Graves T., Harmon G., Edwards J.,
RA Kerlicki J., Schott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Scott K., Johnson D.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
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P24806; O39148; Q41904; O64956;
O1-MAR-1992 (Rel. 21, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medford J.I., Elmer J.S., Klee H.J.;
"Molecular cloning and characterization
apical meristems.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaler B., Mache R., Mueller M., Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE .....
STRAIN=cv. Columbia;
STRAIN=cv. Tomita E.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core «
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MERI-5 protein precursor (Endo-xyloglucan transferase) (Xyloglucan endo-1,4-beta-D-glucanase).
MERI-5 OR MERI5B OR SEN4 OR AT4G30270 OR F9N11.120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Columbia; Arrowsmith D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=93005704; PubMed=1840916;
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                                                                                                     Query Match
Best Local S
Matches 47
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EMBL, D63508; BAA09783.1; -

EMBL, AL109996; CAB52471.1; -

EMBL; AL161576; CAB81020.1; -

EMBL; AV035156; AAK59660.1; -

EMBL; AV039027; AAK59600.1; -

EMBL; AV063027; AAK59601.1; -

EMBL; AV063027; AAC39467.1; -

EMBL; AF035384; AAC39467.1; -
                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Mol. Biol. 37:445-454(1998).

-!- FUNCTION: INVOLVED in cell wall reconstruction.
-!- TISSUE SPECIFICITY: EXPRESSED IN SHOOT APICAL MERISTEMS, ALSO FOUND IN SEEDLINGS AND MERISTEMS.
-!- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
-!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 158; 178; 183; 189; 190; 194 and 199.
-!- CAUTION: Ref.6 sequence differs from that shown due to frameshifts in positions 93 and 104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M., Martlenssen R., McCombie W.R.; "Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-cv. Columbia; Shinozaki K., Davis R.W., Ecker J.R., Theol Shinozaki K., Davis R.W., Ecker J.R., Theol "RIKEN Arabidopsis full length cDNA clones SSP consortium (Salk/Stanford/PGEC)."; Submitted (NOV-2001) to the EMBL/GenBank/DE
                                                                                                                                                                   Glycosidase;
SIGNAL
                                                                                                                                                                                                                                                    PIR; JQ1022; JQ1022.
HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Park J.-H., Oh S.A., Kim Y.H., Woo H.R., Nam H.G.; "Differential expression of senescence-associated misenescence induced by different senescence-inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98278374; PubMed=9617812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia; T1 Raynal M., Grellet F.,
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                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis.";
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SGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGK-
                                                                                                                                                                                             Pro; IPR000757; Glyco_hydro_16.
PF00722; Glyco_hydro_16; 1.
TE; PS01034; GLYCOSYL_HYDROL_F16;
                                    l Similarity
47; Conser
                                                                                              22
93
184
269
                                    Conservative
                                                                                                                                                                                 Hydrolase; Signal
                                                                                                   AA;
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269
94
184
                                                                                                  30755 MW;
                                                 11.3%;
26.3%;
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., Laudie M., Meyer Y., Cooke R., D
to the EMBL/GenBank/DDBJ databases
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                                    34;
                                                Score 150.5;
Pred. No. 1.
                                                                                              MERI-5 PROTEIN.
GS -> DR (IN REF. 7).
A -> G (IN REF. 1).
; 648F042BC7ADED86 CRC64;
                                                                                                                                                                   POTENTIAL
                                  Mismatches
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lones (RAFLs) sequenced
                                                 4e-05
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                                                                 Length
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RESULT 13

UTR2_YEAST
ID UTR2_YEAST
AC 93623;
DT 01-0CT-1994 (Rel. 3
DT 01-0CT-1996 (REB-1993)
RN 12
RN SEQUENCE FROM N.A.
RA Mulligan J.T., Diet
RA MILLIGAN J.T., Diet
RA MILLIGAN J.T., Diet
RA MILLIGAN J.T., Diet
RA MILLIGAN J.T., Diet
RA SEQUENCE FROM N.A.
RC STRAIN-5288C / AB97
RA DIETICH F.S., Mull
RA Chung E., Berno A.
RA Chung E., Duncan M.
RA Hyman R., Kayser A.
RA Mosedale D., Nakaha
RA Mosedale D., Nakaha
RA Hyman R., Kayser A.
RA Hyman R., Kayser A.
RA Mosedale F.S., Roberts
RA Taylor F., Wei Y.,
RL SUDENCE FROM N.A.
RC STRAIN-9-6441;
RA MEDILINE-94016558;
RE MEDILINE-94016558;
RA MEDILINE-94016558;
RA MEDILINE-94016558;
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of Saccharomyces cerevisiae share a con
J. Mol. Biol. 233:372-388(1993).
-i- SIMILARITY: SONE, TO YEAST YGR189C
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Ara Dietrich F.S., Berno A., Brennan T., Carpenter J., Chen E., Che Aviles E., Berno A., Brennan E., Hartzell G., Hunicke-Smith Chung E., Duncan M., Guzman E., Hartzell G., Lew H., Lin D., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was the second of the second of
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U18779; AAB65002.1; ALT_INIT.
EMBL; L22173; AAA34941.1; -.
EMBL; S65964; AAD13975.1; -.
EMBL; S66130; AAB23444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The gene clusters ARC and COR on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Sm Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UTR2 protein (Unknown transcript 2 UTR2 OR YEL040W OR SYGP-ORF18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
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                                                                                                                                                                                                                                            _hydro_16.
                      SER-RICH.
POLY-SER.
L -> V (IN |
A -> R (IN |
S -> C (IN |
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Cherry J.M.,
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 32, Created)
16-OCT-2001 (Rel. 32, Last sequence update)
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                                        CHAIN
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pfam; pF00722; Glyco_hydro_16; 1.
pROSITE; PS01034; GLYCOSYL_HYDROL_F1
                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spilliaert R., Hreggyidsson G.O., Kristjansson J.K., Eggertsson G., Palsdottir A.; "Cloning and sequencing of a Rhodothermus marinus gene, for a thermostable beta-glucanase and its expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
7215C33624135191 CRC64;
                                                                                                                                               POTENTIAL
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                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and characterization of a brassinosteroid-regulated gene from elongating soybean (Glycine max L.) epicotyls."; Plant Physiol. 104:161-170(1994).
-!- FUNCTION: POSSIBLE ROLE IN BRASSINOSTEROID-STIMULATED ELONGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max (Soybean).

Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida

eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycosidase; Hydrolase; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L22162; AAA81350.1; -. HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00722; Glyco_hydro_16; 1
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94159788; PubMed-8115544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Epicotyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zurek D.M., Clouse S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDFSGAELYTLEEVQ--YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV---EVDI
ADGRPWVEVDIEVLGK---NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEW 105
                                                                                                                                                               AKDFSGAELYTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRVYRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGQEVRKTEGGQVSNLTG-----TQGLRFNLWSSESAAWVGQ--FDESKLPLFQFINW 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REYTSARLVTRGKASWTYGRFEIRARLPSGRGTWPAIWMLPDRQTYGSAY-WPDNGEIDI 161
                                                                                 AKIFNGGQLLSLSLDKVSGSGFKSKKEYLFGRIDMQLKLVAGNSAGTVTAYYL-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDSLYYRFPNERLTDPEADWRHWPFDQPFHLIMNIAVGGAWGGQQGVDPEAFPAQLVVDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -EVLGKNP---
                                                                                                                                                                                                                                        l Similarity
46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000757; Glyco_hydro_16
                                                                                                                                                                                                                                                                                                                                                                                                   283 AA;
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        31
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                                                                                                                                                                                                                                                                                                                                                                                                   32254 MW;
                                                                                                                                                                                                                                                                         9.6%;
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23.7%;
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                                                                                                                                                                                                                                        Pred. No. 0.0
l; Mismatches
                                                                                                                                                                                                                                                                             Score 128; DB 1;
Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                        BRASSINOSTEROID-REGULATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 133.5; DB : Pred. No. 0.00038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                       EEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEI 48
                                                                                                                                                                                                                                                                                                                                                                                                   C248810EC7835737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                            73;
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                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaborationMBL outstation
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                                                                                     98
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BRU1_SOYBN
CGKA_ALTCA
E13B_BACCI
ALGE_PSEAE
VP4_ROTPC
GUN5_BACAG
C5AC_BACTU
C5AA_BACUD
VM21_BORHE
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	278 278 285 292 301 349 AA;	23904; 1AJK. 0; IPRO00757; F00722; Glyco; F801034; GL; se; Glycosida 1 28 3 28 3 28 3 28 3 27 3	e Swiss in Bioin n-profi ind this equires email to	ENCE FROM N.A., AND SEQUENCE O INN=150late 585; INN=590299807; PubMed=2193918; her R.M., Erfle J.D.; sequence of a Fibrobacter suc- glucanase (1,3-1,4-beta-D-glu acteriol 172:3837-3841(1990). CATALYTIC ACTIVITY: Hydrolysis in beta-D-glucans containing SIMILARITY: BELONGS TO FAMILY	(Re (Re (Re Ese Se Lic Suc Suc	
2	73	1AJK. 0000757; Glyco 000757; Glyco_hydr 034; GLYCOSY 9cosidase; \$ 1 27 28 349 79 79 79 79 70 377	Insti Insti format format format t ins t ins statem a lice o lice o lice	N.A., AND SEQUENCE S85; FUDMed=2193918 Erfle J.D.; of a Fibrobacter s (1,3-1,4-beta-D-9 172:3837-3841(1990 ACTIVITY: Hydrolys BLONGS TO FAMILE BELONGS TO FAMILE 1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	STANDARD; 1. 16, Creal 1. 16, Lass 1. 38, Lass precursor -glucan 4 henase). cinogenes bacter/Aci	287 2889 361 422 1531 1545 1546 1549 1549 1103
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                             CHAIN
ACT_SITE
ACT_SITE
                                                                                                       Hydrolase;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
01-JUN-1994 (Rel. 29, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
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P37073;
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Appl. Microbiol. Biotechnol. 38:507-51:
  SEQUENCE
                                                                                                                                                       PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                 EMBL; M84339; AAA22265.1; -. HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE-93159752; PubMed-7763386;
LOUW M.E., Reid S.J., Watson T.G.;
"Characterization, cloning and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus brevis.
Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L. MICTOBLOL. BIOLECHNOL. 38:507-513(1993).

FUNCTION: HYDROLYSES B-GLUCANS CONTAINING MIXED BETA-1,3 AND BETA-1,4 LINKAGES. THIS ENZYME IS THERMOSTABLE; ITS OPTIMAL TEMPERATURE IS NEAR 65-70 DEGREES CELSIUS.

CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.

MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGE SIMILAR TO LICHENASE OF GERMINATING BARLEY.

SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACBR
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                                                                                                                                                                                                              PF00722; Glyco_hydro_1
                                                                                                                                                                                                                                      IPR000757; Glyco_hydro_16
                                                                                                         Glycosidase;
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                                                                                                                                  Signal
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BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
A63C09F281FF5D13 CRC64;
                                                                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoshida K.-I., Shindo K., Sano H. Miwa Y., Fujita Y.;
"Sequencing of a 65 kb region of containing the lic and cel loci, covering the gnt-sacXY region.";
Microbiology 142:3113-3123(1996)
      J. Bacteriol.
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STRAIN=168 / BGSCIA1;
MEDLINE=97124196; PubMed=8969509;
MEDLINE=97124196; PubMed=8969509;
MEDLINE=97124196; PubMed=8969509;
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Tezuka H., Yuuki T., Yabuuchi S.;
"Construction of a beta-glucanase hyperproducing Bacillus subtilis
"Construction of a beta-glucanase gene and a multi-copy plasmid.";
using the cloned beta-glucanase gene and a multi-copy plasmid.";
aaric. Biol. Chem. 53:2335-2339(1989).
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                                                                                                           Rak
                                                                                                                                                                                                                                                                                                     "Genes encoding xylan and beta-glucan hydrolysing enzymes in subtilis: characterization, mapping and construction of straideficient in lichenase, cellulase and xylanase."; Microbiology 141:281-290(1995).
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Bacteria; Firmicutes;
                                                                                                                                      Schnetz K.,
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                                                                     Bacillus
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                                                                                                                                      78961; PubMed=8606172; Stuelke J., Gertz S.,
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EMBL; D00518; BAA10697.1; -.
EMBL; Z46862; CAA86922.1; -.
EMBL; Z29340; CAA86922.1; -.
EMBL; Z299124; CAB15943.1; -.
EMBL; Z299124; CAB15943.1; -.
EMBL; Z29914; LXBS.
PIR; JU0110; JU0110.
HSSP; P27051; 1GBG;
SubtiList; BG10476; bg1S.
InterPro; IPR000757; Glyco_hydro_16; 1.
PRINTS; PR00737; GLYCo_hydro_16; 1.
PRINTS; PR00737; GLYCO_SYL_HYDROL_F16; 1.
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                                                                                                                                                    VSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                        TKVQFNYYTNGAG----NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHTATNQ
                                                                                                                                                                                                               FDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPT---DGTPWDEIDIEFLGKDT 143
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                    Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               204
242 AA;
                                         (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                    133
137
137
24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-63.
                                                                                                                                                                                                                                                        Conservative
                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                          28
242
29
133
137
89
24
24
204
27268
35, Created,
35, Last sequence update,
41, Last annotation update,
ucanase precursor [Includes: Endo-1,4-beta-xylanase
                                                                                                                                                                                                                                                                 17.1%;
35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                  Signal;
                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY)
BY SIMILARITY.
BY SIMILARITY.
A -> S (IN STRAIN HL-25).
A -> L (IN STRAIN C120).
                                                                                                                                                                                                                                                                  Score 245.5;
Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                BETA-GLUCANASE.
                                                                                PRT;
                                                                                                                                                                                                                                                                                               -> S (IN STRAIN HL-25).
-> S (IN STRAIN HL-25).
-> L (IN STRAIN C120).
45958DEA70F22B29 CRC64;
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
                                                                                802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                   .8e-13
                                                                                Ŗ
                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
                                                                                                                                                                                                                                                       71;
                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                        Indels
                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta-glucanase
                                                                                                                                                                                                                                                                            242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is
ifor
                                                                                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
                                                                                                                                                                                                                                                       Gaps
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Query Match
Best Local S
Matches 58
                                                                                                         ACT_SITE
ACT_SITE
ACT_SITE
                                                                   DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                        PRINTS; PRO0911; GLHYDRLASE11.
PRINTS; PRO0737; GLHYDRLASE16.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2;
PROSITE; PS00777; GLYCOSYL_HYDROL_F16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                         InterPro; IPR001137; GH_11.
InterPro; IPR000757; Glyco_hydro_16; ffam; PF00457; Glyco_hydro_11; 1.
pfam; PF00722; Glyco_hydro_16; 1.
pfam; PF02018; CBM_4_9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 175:2943-2951(1993).
i- FUNCTION: CONTAINS TWO CATALYTIC DC
BETA-1,3-1,4 GLUCANASE ACTIVITIES.
-i- CATALYTIC ACTIVITY: Endohydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALÝTIC ACTÍVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
-!- PATHWAY: Xylan degradation.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMI: G (FAMILY 11 OF GLYCOSYL HYDROLASES).
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93259938; PubMed=8491715; Flint H.J., Martin J., McPherson C.A., Daniel A.S., Zhang J.-X.; Flint H.J., Martin J., McPherson C.A., Daniel A.S., Zhang J.-X.; Abifunctional enzyme, with separate xylanase and beta(1,3-1,4)-glucanase domains, encoded by the xynD gene of Ruminococcus
                                                      SEQUENCE
                                                                                                                                                 DOMAIN
                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucanase domains, flavefaciens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruminococcus flavefaciens.
Bacteria; Firmicutes; Clostridia;
                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                              Xylan
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S61204; AAB26620.1; HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XYND.
                                                                                                                                                                                                                                 Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EC 3.2.1.8) (Xylanase): Endo-beta-1,3-1,4 glucanase (EC 1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linkages in xylans.
                                                                                                                                                                                                                                            degradation; Hydrolase;
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                              IPR003305; CBM_CenC.
  Conservative
                                                      AA;
                                                                                                                                                                                                                enzyme.
                                                                    89091 MW;
              16.9%;
 21;
                                                                                                                                                LINKER.
C (BETA
Pred. No. 1.3
                            Score
                                                                   NUCLEOPHILE (BY SIMILARITY).
POLY-THR.
POLY-THR.
POLY-THR.
                                                                                                                     C (BETA-GLUCANASE).
NUCLEOPHILE (BY SIMILARITY)
PROTON DONOR (BY SIMILARITY)
                                                                                                                                                                                                     XYLANASE/BETA-GLUCANASE
                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                              Glycosidase;
                                                                                                                                                                                       (XYLANASE).
                                                      2880A689647284AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridiales;
                            242.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAINS WITH XYLANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 1,4-beta-D-xylosidic
                .3e-1
                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as its content
                                                                                                                                                                                                                                            Signal;
                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lachnospiraceae;
                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.2.1.73)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D
 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 outstation
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 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUB_BACAM
P07980;
01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-87192007; PubMed-3106158;
MEDLINE-87192007; Nurtz A., Borriss R., Knowles J.;
"The beta-glucanase gene from Bacillus amyloliquefaciens shows extensive bomology with that of Bacillus subtilis.";
Gene 49:177-187(1986).
-1 CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
-1 MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGI SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-1 SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M15674; AAA87323.1;
PIR; A29091; A29091.
HSSP; P27051; 1GBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ol-JUN-1994 (Rel. 29, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1988 (Rel.
01-AUG-1988 (Rel.
01-JUN-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus amyloliquefaciens.
Bacteria; Firmicutes; Bacil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BE 20/78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1390;
     193
                                                      123
                                                                                                         137
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                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                       SYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDIEFL 136
                                                                                                                                                                                                                                        SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL
ATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYDWMRYRK
                                                                                                      GKDTTKVQFNYYTNGAG----NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHT
                                                                                                                                                       GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQDIPKTPGKIMMNAWPGLTVDDWLKAFN-GRTPLTAHYQWVTYNK
                                                   EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSNLTGTQG-LRENLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
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                                                                                                                                                                                                                                                                                                                   58;
                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000757; Glyco_hydro_16
0722; Glyco_hydro_16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  26
134
57
239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycosidase;
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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08, Last sequence update)
29, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                25
239
134
86
                                                                                                                                                                                                                                                                                                                                                                                                                       26928
                                                                                                                                                                                                                                                                                                                                         16.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -EKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                      Score 238.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  A76A64268A7AAA0B CRC64;
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
                                                                                                                                                                                                                                                                                                                                         .6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170
                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucanase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collaboration .
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                      192
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RESULT 6
GUB_CLOTM
ID GUB_CLOTM
ID GUB_CLOTM
ID GUB_CLOST
AC P2971
DT 01-FE
DE Bacte
OC Clost
OC STRAI
RX MEDLI
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P29716; P37074;
01-APR-1993 (Rel. 2
01-JUN-1994 (Rel. 2
01-FEB-1996 (Rel. 3
                                                                                                                                                                  PIR; S23498; S23498.
PIR; JS0611; JS0611.
PIR; S18726; S18726.
HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning the Clostridium thermocallum thermostable laminarinase gen
in Escherichia coli; the properties of the enzyme thus produced.";
Biotechnol. Lett. 12:811-816(1990).

-i- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkage
in beta-D-glucans containing 1,3- and 1,4-bonds.

-i- SUBUNIT: MAY FORM PART OF A MULTIENZYME COMPLEX (CELLULOSOME).

-i- DOMAIN: A 24 RESIDUES DOMAIN IS REPEARED TWICE IN THIS ENZYME &
WELL AS IN OTHER C.THERMOCELLUM CELLULOSOME ENZYMES. THIS DOMAIN MAY FUNCTION AS THE BINDING LIGAND FOR THE SL COMPONENT.
InterPro; IPR002105; Dockerin_1.
InterPro; IPR002048; EF-hand.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00404; Dockerin_1; 2.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              EMBL; X63355; CAA44959.1; -. EMBL; X58392; CAA41281.1; -.
                                                                                                                                                                                                                                                                                                                                          or send an
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STRAIN-ATCC 27405 / DSM 1237;
MEDLINE-92155194; PubMed-1740123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium thermocellum.
Bacteria; Firmicutes; Clostridia;
                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-F7
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Zverlov V.V., Laptev D.A., Tishkov V.I., Velikodvorskaja
"Nucleotide sequence of the Clostridium thermocellum lam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lichenases joined to cellulases.";
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lucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
,4-beta-D-glucan 4-glucanohydrolase) (Lichenase) (Laminarinase).
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SIGNAL
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                                                                                                                                                      MEDLINE=91224124; PubMed=2026156; MEDLINE=91224124; PubMed=2026156; J.A., Querol E.;
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01-AUG-1992 (Rel. 23, Last
01-NOV-1997 (Rel. 35, Last
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         Planas A., Juncosa M., Lloberas J., 
"Essential catalytic role of Glu134 
glucanohydrolase from B. licheniforn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                         MEDLINE=92362869;    PubMed=1354172;
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EC 3.2.1.73) (Endo-beta-1,3-1,4
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PROTON DONOR (BY SIMILARITY).
PRO/THR-RICH (LINKER).
2 X 24 AA APPROXIMATE REPEATS
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      endo-beta-1,3-1,4-D-glucan as determined by site-dired
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEBS Lett. 374:221-224(195).

-i- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic in beta-D-glucans containing 1,3- and 1,4-bonds.
-i- MISCELLANEOUS: 3ETA-GLUCANASES OF BACILLUS HAVE A SUBSTR.
SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-i- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Crystal structure of Bacillus lichenif glucanohydrolase at 1.8-A resolution."; FEBS Lett. 374:221-224(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94237863; PubMed=8182059;
Juncosa M., Pons J., Dot T., Querol E., Planas A.;
"Identification of active site carboxylic residues in Licheniforms 1,3-1,4-beta-D-glucan 4-glucanohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SÍGNAL
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PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
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J. Biol. Chem. 269:14530-14535(1994).
                                                                                                                                                                                                         SEQUENCE
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Hahn M., Pons J., Planas A., Quer
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EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
                                        GKDTTKVQFNYYTNGVG---NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-LKHT
                                                                                             SYNKFDCGENRSVQTYGYGLYEVNMKPAKNVGIVSSFFTYTGPT---DGTPWDEIDIEFL
                                                                                                                        SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL
                                                                   GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT
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                                                                                                                                                      Conservative
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7; GLHYDRLASE16
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179
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33.7%;
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N: 85% OF WILD-TYPE ACTIVITY.
D: 38% OF WILD-TYPE ACTIVITY.
D: 50% OF WILD-TYPE ACTIVITY.
N: 15% OF WILD-TYPE ACTIVITY.
D: 0.2% OF WILD-TYPE ACTIVITY.
D: 0.2% OF WILD-TYPE ACTIVITY.
D: 0.5% OF WILD-TYPE ACTIVITY.
D: 15% OF WILD-TYPE ACTIVITY.
                                                                                                                                                                                                                                   COMPLETE LOSS OF A

65% OF WILD-TYPE A

15% OF WILD-TYPE A

60% OF WILD-TYPE A

80% OF WILD-TYPE A

70% OF WILD-TYPE A
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No 3.8e-12;
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(See http://www.isb-sib.ch/announce/
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ic residues in Bacillus
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L outstation -
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PAEMA
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01-JUN-1994
15-JUL-1998
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"Crystal
Bacillus
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P23904;
                                                                PIR;
PDB;
PDB;
PDB;
PDB;
                                                                                                                               EMBL;
                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93094208; PubMed-1360982; Hood P.B., Condron R., Traeger J.C., McA "Identification of glutamic acid 105 at amyloliquefaciens 1,3-1,4-beta-D-glucan epoxide-based inhibitors."; J. Biol. Chem. 267:25059-25066(1992).
                                                                                                                                                                                                                                     This
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MEDLINE-96028129; PubMed-7588726;
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93281743; PubMed=8099449;
Keitel T., Simon O., Borriss R.,
"Molecular and active-site struct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
Paenibacillus macerans (Bacillus macerans).
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Pae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Beta glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borriss R., Buettner K., Maentsaelae P.; "Structure of the beta-1,3-1,4-glucanase homelogies to other beta-glucanases."; Mol. Gen. Genet. 222:278-283(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-91109712; PubMed-2274030;
              interPro;
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CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic in beta-D-glucans containing 1,3- and 1,4-bonds.

MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTR SIMILAR TO LICHENASE OF GERMINATING BARLEY.

SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                         European Bioinformatics Institute.
                        1AJK;
1AJO;
                                                  1CPM;
1CPN;
1MAC;
                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                           1BYH;
 PF00722;
                                                                                                                               x55959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1990),
                                                                                                                                                                                                                                                                                                                    Keitel T., Heinemann U.; and molecular structure at 0.16-nm resolution endo-1,3-1,4-beta-D-glucan 4-glucanohydrolase Biochem. 232:849-858(1995).
                      27; S11927.
31-MAR-95.
31-WAR-95.
22-JUN-94.
22-JUN-94.
22-JUN-94.
27-FEB-95.
06-MAY-98.
             IPR000757;
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                                                                                                                               CAA39426.1;
00757; Glyco_hydro_16.
Glyco_hydro_16; 1.
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e-site structure of a Bacillus 1,3-1,4-beta-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McAuliffe J.C., Stone at the active site of can 4-glucanohydrolase
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                                                                                                                                                                     (See http://www.isb-sib.
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Matches 59
                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last squence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4
[1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
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     Bacteria; Firmicutes;
             Paenibacillus
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                                                                                                            192
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                                                                                                                    VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT
                                                                                                            TANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV----KYT
                                                                                                                                       TKVQFNYYTNGVGGH---
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                                                                                                                                                                    FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDIEFLGKDT 138
                                                                                                                                                                                 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                Similarity
59; Conserv
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                                                                                                                                                                                                 Conservative
           polymyxa
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     (Bacillus
Bacillales;
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                                                                                                                                                                                                       Score 226;
Pred. No. 7.
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NUCLEOPHILE (BY SIMILARITY)
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    polymyxa).
; Paenibacillaceae;
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                                 glucanase)
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                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endo-1,3-1,4-beta-glycanase exoK precursor (EC biosynthesis protein exoK).
EXOK OR RB1080 OR SMB20955.
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ACT_SITE
DISULFID
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SEQUENCE FROM
STRAIN=ATCC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gosalbes M.J., Perez-Gonzalez J.A., Gonzalez R., Navarro A.; "Two beta-glycanase genes are clustered in Bacillus polymyxa: molecular cloning, expression, and sequence analysis of genes encoding a xylanase and an endo-beta (1,3)-(1,4)-glucanase."; J. Bacteriol. 173:775-7710(1991).
                                                                      Rhizobium meliloti (Sinorhizobium meliloti). Plasmid pSymB (megaplasmid 2). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                      RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as lits content is in no way
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-:- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
-:- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
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   MEDLINE=94042869;
                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                    TKVQFNYYTNGVGGH----EKIINLGFDASTSFHTYAFDWQPGYIKWYVDG-VLKHT---A
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   PubMed=8226645
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34.5%;
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 225;
Pred. No. 8.
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                                                                                                                                                                                                                                     PRT;
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                                                                                      subdivision;
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                                                                                                                                                         3.2.1.-) (Succinoglycan
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Best Local
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depolymerize nascent succinoglycan chains.";

Proc. Natl. Acad. Sci. U.S.A. 95:4912-4917(1998).

-i- FUNCTION: CLEAVES HIGH MOLECULAR WEIGHT SUCCINOGLYCAN TO YIELD LMW

SUCCINOGLYCAN. DYNAMICALLY REGULATE THE MOLECULAR WEIGHT

DISTRIBUTION OF SUCCINOGLYCAN BY CLEAVING NASCENT SUCCINOGLYCAN

ONLY DURING A LIMITED PERIOD AFTER ITS SYNTHESIS, PERHAPS BEFORE

ONLY DURING A LIMITED PERIOD AFTER ITS CONFORMATION OR
                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as a use by non-profit institutions as long as i modified and this statement is not removed. Usentitles requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Family of glycosyl transferases needed succinoglycan by Rhizobium meliloti."; J. Bacteriol. 175:7033-7044(1993).
                                                                                                                                                                                                                                                          InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                   SIGNAL
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MEDLINE=98226741; FubMed=9560202;
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Vorhoelter F.J., Hernan
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MEDLINE=93241147; PubMed=8479421;
                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                   Complete
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                                                                                                                                                                                                                                                                                                      HSSP; P23904; 1AJK
                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                              Exopolysaccharide synthesis; Glycosidase; Hydrolase; Signal; Plasmid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Analysis of the Rhizobium meliloti exoH/exoK/exoL fragment: Exol
shows homology to excreted endo-beta-1,3-1,4-glucanases and ExoH
resembles membrane proteins.";
Mol. Gen. Genet. 238:145-154(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
            62 LGKNPGSFQSN-IITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Exopolysaccharide biosynthesis.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONES TO FAMILY 16 OF GLYCOSYL HYDROLASES.
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                                                                     VSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEV
                                          VKERNFACGEIQTFKRFGYGTYEARIKAADGSGLNSAFFTYIGP---ADKKPHDEIDFEV
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                                                                                                   Conservative
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93
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Hernandez-Lucas
                                                                                                                  13.7%;
32.5%;
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                                                                                                                                                          MW;
                                                                                                   31;
                                                                                                               Score 197; 1
                                                                                                 Pred. No. 2.2
L; Mismatches
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ACGEIQTRKR -> LRRNPDAQG (IN
073CC7ED65EF2611 CRC64;
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Cowie A.,
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DOMAIN 63 66
DOMAIN 301 310
DOMAIN 345 355
DOMAIN 387 391
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Ol-OCT-1996 (Rel. 34, Last sequence update)
Ol-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 52.8 kDa protein in BUB1-HIP1 in
YGR189C OR G7553.
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or send a
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EMBL; X99074; CAA67525.1; -.
HSSP; P23904; 1AJK.
SGD; S0003421; CRH1.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Saccharomyces cerevisiae Yeast 13:357-363(1997).
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Arroyo J., Garcia-Gonzalez M., Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).

Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                            SEQUENCE
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VIVTDYSTGKKYTYGDQSGSW-ESIEADGGSIYGRYD
                        VKVYKYTPGQGEGGSDFTLDWTDNFDTFDGSRWGKGD
                                                                              KTEGGQVSNLTGTQG-----LRFNLWSS---ESAA----WV-GQFDESKLPLFQFINW
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                                                                                                                                    VLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVR 120
                                                                                                                                                                MTLAKRYDNPSLKSNFYIMYGKLEVILKAANGTGIVSSFYLQSDDLD-----
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non-profit institutions as long as its content is in
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POLY-SER.
POLY-SER.
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Pred. No. 7.
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RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
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RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koethert R.,
RA Dese S., Hempel S., Feldpausch M., Lanberth S., De Clercq R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pose S., de Haan M., Maarse A.C., Schaefer M., Gelmert T.-H.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Chinabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schnocking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Kramer J., Fullton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fullton B., Miller N., Greco T., Kemp K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDIJINE=93005704; PubMed=1840916;
Medford J.I., Elmer J.S., Klee H.J.;
"Molecular cloning and characterizat
apical meristems.";
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MERI-5 OR MERI5B OR SEN4 OR AT4G30270 OR
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01-MAR-1992 (Rel. 21, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert Pohl T., Duesterhoeft A., Stiekema W., Entlan K.-D., Terryn K. Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mue Weichselgartner M., de Simone V., Obermaier B., Mache R., Mue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Columbia; Arrowsmith D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-cv. Columbia;
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Matches 47
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STRAIN-CV. Columbia; TISSUE-Leaf;
MEDLINE-98278374; PubMed-9617812;
Park J.-H., Oh S.A., Kim Y.H., Woo H.R., Nam H.G.;
Poifferential expression of senescence-associated mR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Columbia; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced SSP consortium (Salk/Stanford/PGEC)."; submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. Columbia; TISSUE-Green siliques;
STRAIN-CV. Columbia; TISSUE-Green siliques;
STRAIN-CV. Grellet F., Laudie M., Meyer Y., Cooke R., De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M., Martienssen R., McCombie W.R.; "Sequence and analysis of chromosome 4 of the plant Arabidopsis thatians"
                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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L; D6308; BAA09783.1; -.

L; AL109796; CAB52471.1; -.

L; AL161576; CAB81020.1; -.

L; AY035156; AAK5960.1; -.

L; AY063027; AAL34201.1; -.

L; AY063027; CAA79012.1; ALT_FRAME.

L; AF0535384; AAC39467.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAUTION: Ref. 1 sequence differs from that shown due in positions 158; 178; 183; 189; 190; 194 and 199. CAUTION: Ref. 6 sequence differs from that shown due in positions 93 and 104.
                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                           JQ1022; JQ1022.
; P23904; 1AJK.
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SGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGK-
                                                                                                                                                                Pro; IPR000757; Glyco_hydro_16.
PF00722; Glyco_hydro_16; 1.
TE; PS01034; GLYCOSYL_HYDROL_F16;
                           47; Conser
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22
93
184
269
                              Conservative
                                                                                                                                                    Hydrolase; Signal
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94
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30755
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26
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                                                                                   WW;
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Pred.
                                                                               MERI-5 PROTEIN.
GS -> DR (IN REF. 7).
A -> G (IN REF. 1).
; 648F042BC7ADED86 CRC64;
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                            Mismatches
                                         150.5;
No. 1.6
                                           .6e-05;
                                                      DB 1;
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RESULT 13
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UTR2_YEAST
P32623;
01-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mocdalo
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01-OCT-1996 (Rel. 34, Last annotation
UTR2 protein (Unknown transcript 2 pro
UTR2 OR YELO4OW OR SYGP-ORF18.
                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb~sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of Saccharomyces cerevisiae sha
J. Mol. Biol. 233:372-388(1993)
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Dietrich F.S., Mulligan J.T.,
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Mulligan J.T., Die
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"The gene clusters ARC and COR on
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Taylor P., Nakahara K., Roberts D., D
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ter J., Chen E.,
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RESULT 14
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GUB_RHOMR
P45798;
                ACT_SITE
                                                       Hydrolase;
SIGNAL
                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                      col1.
                                                                                                                                                                                                                                                                                                                                                                                                  Spilliaert R., Hreggvidsson G.O., Kristjansson J.K., Eggertsson G., Palsdottir A.; "Cloning and sequencing of a Rhodothermus marinus ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    for a
  SEQUENCE
                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=21 / ITI-378;
MEDLINE=95010084; PubMed=7925416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodothermus marinus (Rhodothermus obamensis).
Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales.
                                                                                     PROSITE;
                                                                                                    fam;
                                                                                                                              EMBL; U04836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=29549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crenotrichaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              v
                                                                                                                                                                                                                                                                 FUNCTION: SHOWS ACTIVITY ON LICHENAN, BETA-GLUCAN AND LAMINARIN BUT NOT ON CMC CELLULOSE OR XYLAN. THE ENZYME HAS A TEMPERATURE OPTIMUM OF 85 DEGREES CELSIUS AND A PH OPTIMUM OF 7.0. CATALYTIC ACTIVITY: Hydrolysis of 1.4-beta-D-glycosidic linkages in beta-D-glucans containing 1.3- and 1.4-bonds. SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPGYYYAIVNEVNITCYDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLETAQTNFYWESVLNYTNSANISTTD------TFENYHTYELDWHEDYVTWSIDGV 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGRTLYKNETYNAT-TQKYQYPQTPSKVDISIWPGGNSTNAPGTIAWSGGEINWDASDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVRKTEGGQVSNLTGTQGLRF-----NLW---SSESA----AWVG---QFDESKLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNSGGTVLSSTRAVWYGKVSARIKTSHLAGVVTGFILYSGAGD------ELDYEFVGA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGK 64
                                                                                                    PF00722;
                                                                                                                                                                                                                                                                                                                                                                                  thermostable beta-glucanase and
                                                                                                                                                                                                                                                                                                                                                         Biochem. 224:923-930(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 25.:
50; Conservative
                                                                                00722; Glyco_hydro_16; 1.
PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                              IPR000757; Glyco_hydro_16
                                                                      Glycosidase;
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                                                                                                                             AAA60459.1; -
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                286
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BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
7215C33624135191 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 147;
Pred. No.
                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                    marinus gene, expression in
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Escherichia
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P35694;
                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                    gene from elongating soybean (Glycine max L.) epicotyls.";
Plant Physiol. 104:161-170(1994).
-i- FUNCTION: POSSIBLE ROLE IN BRASSINOSTEROID-STIMULATED EI
-i- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                 Zurek D.M., Clouse S.D.;
Zurek D.M., Clouse S.D.;
"Molecular cloning and characterization of a brassinosteroid-regulated
"Molecular cloning and characterization of a brassinosteroid-regulated
aene from elongating soybean (Glycine max L.) epicotyls.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
                                                                                                                                   SIGNAL
                                                                                                                                                             Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                      EMBL; L22162; AAA81350.1;
HSSP; P23904; LAJK.
                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassinosteroid-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOYBN
                                                                                                           SEQUENCE
                                                                                                                        CHAIN
                                                                                                                                                 Glycosidase; Hydrolase; Signal
                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94159788; PubMed=8115544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel.
                                                                                                                                                                                         InterPro; IPR000757; Glyco_hydro_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166
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AKIFNGGQLLSLSLDKVSGSGFKSKKEYLFGRIDMQLKLVAGNSAGTVTAYYL-----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEHVGFNPDVVHGTVHTKAYNHLLGTQRGGSIR---VPTARTDFHVYAIEWTPEEIRWFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REYTSARLVTRGKASWTYGRFEIRARLPSGRGTWPAIWMLPDRQTYGSAY-WPDNGEIDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDSLYYRFPNERLTDPEADWRHWPFDQPFHLIMNIAVGGAWGGQQGVDPEAFPAQLVVDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                     46;
                                                                 Similarity
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                                                     Conservative
                                                                                                          AA;
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                                                                                                       283
32254 мw;
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                                                                  8.98;
23.78;
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                                                                 Score 128;
Pred. No. 0
                                                                                                       BRASSINOSTEROID-REGULATED; C248810EC7835737 CRC64;
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                      -EEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEI
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                                    DB 1
0.0013;
's 73;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
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Q15691 bacillus su
Q8fmg0 bacillus su
Q9ffdc9 paenibacill
Q07856 streptococc
Q93uil uncultured
Q97fd3 clostridium
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ALIGNMENTS

A CONTRACTOR OF THE CONTRACTOR Query Match Best Local S Matches SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; FubMed=11058132;
MEDLINE=20512582; FubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Marakami F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28:4317-4331(2000).

EMBL; AP001518; BAR06951.1; HSSP; P23904; IAJK.
InterPro; IPR001757; Glyco_hydro_16.
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00722; Glyco_hydro_16; 3.
Pfam; PF00746; Gram_pos_anchor; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 3. Q9K7X5; 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, Hydrolase; SEQUENCE Endo-beta-1,3-1,4 glucanase BGIS OR BH3222 Bacillus halodurans. Bacteria; Firmicutes; Bacill Bacillaceae; Bacillus. NCBI_TaxID=86665; Q9K7X5 21 LTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEV 80 l Similarity 83; Conserv Glycosidase; Complete proteome. 851 AA; 98142 MW; ClC4F0F158400285 CRC64; Conservative PRELIMINARY; 14.78; 29.48; Bacillus/Clostridium group; Bacillales; Created)
Last sequence update)
Last annotation update)
(licheninase) (EC 3.2.1.73). Score 268.5; DB 16; Pred. No. 7.2e-10; 12; Mismatches 112; PRT; 851 Ą DB 16; Indels Length 851; Masui subtilis."; 55; z Gaps

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01-DEC-2001 (TrEMBLrel. 1:
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ database.

EMBL; AF306531; AAG53947.1; -.

HSSP; P33904; 1AJK.

InterPro; IPR000757; Glyco_hydro_16.

Pfiam; PF00722; Glyco_hydro_16; 1.

PRINTS: PR00737; GLHYDRALASE16.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.

SEQUENCE 256 AA; 27604 MW; 989E50C09F6E4531 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium
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       Bacillus
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Pred. No. 1.3e-09;
9; Mismatches 71;
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RESULT 4
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Matches 61
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Matches
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Q93GE8;
O1-DEC-2001 (TrEMBLrel. 19, C
O1-DEC-2001 (TrEMBLrel. 19, L
O1-MAR-2002 (TrEMBLrel. 20, L
Endo 1-3,1-4-beta-glucanase uncultured bacterium.
                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
NON_TER
SEQUENCE
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Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOCO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Novel lichenases from soil.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AF254957; AAK50610.2;
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; environmental samples.
NCBI_TaxID=77133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rodriguez V., Mellado R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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EMBL; Z12151; CAA78135.1; -.
HSSP; P23904; 1AJK.
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Santamaria R.I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94288605; PubMed=7517127;
                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                     Match
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                                                                                                                                                                                                                                                                   Similarity
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51; Conservative
                                                                                                                                          TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                     TSPSYNKFDCGENRSVQTYGYGPYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKIQFNYFTNGVGG----NEHYHELGFDAADDFNTYAFEWRPESIRWFVNGELVHTA----
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276 AA;
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Pred. No. 4.3e
20; Mismatches
                                                                                                                                                                                                                              Score 246.5; DB 2;
Pred. No. 3.6e-09;
5; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                                                     3DB186D3B9D991CF CRC64;
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75;
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                                                                                                                                                                                                                                 11;
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01-DEC-2001 (TrEMBLrel. 19, C)
01-DEC-2001 (TrEMBLrel. 19, La
01-MAR-2002 (TrEMBLrel. 20, La
Endo 1-3,1-4-beta-glucanase (I
uncultured bacterium.
                                                          Submitted (FEB-1999) to the EMBL; AJ132472; CAB51934.1; HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridiales; Lachnospiraceae; NCBI_TaxID-1265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Family 11 xylanase /family 16 beta (1,3-1,4) glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RODITIQUEZ V., Mellado R.P.;
"Novel lichenases from soil.";
"Novel lichenases from soil.";
submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AF254959; AAK50612.2;
Interpro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
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                                                                                                                                                 "Organisation and strain utilization of xylans by flavefaciens 17.";
                                                                                                                                                                                                                                     Aurilia V., Martin J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNYX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9S310
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruminococcus flavefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9S310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI
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      IPR003305;
IPR001137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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   CBM_CenC.
GH_11.
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35.5%;
                                                                                                                                                                             by the
                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus/Clostridium
                                                                                                                                                                          Munro C.A., Mercer D.K., Flint H.J.; distribution of genes responsible for the rumen cellulolytic bacterium Rum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                        EMBL/GenBank/DDBJ databases
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Pred. No. 4.2e-09;
5; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                       Ruminococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                      group; Clostridia;
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01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Create 01-DEC-2001 (TrEMBLrel. 19, Last s 01-MAR-2002 (TrEMBLrel. 20, Last a Endo 1-3,1-4-beta-glucanase (Fragmuncultured bacterium.

Bacteria; environmental samples.

NCBL_TaxID=77133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000757; Glyco_hydro_16.

pfam; pF02018; CBM_4_9; 2.

Pfam; pF00457; Glycc_hydro_11; 2.

pfam; pF00722; Glycc_hydro_16; 2.

pRINTS; pR00911; GLEYDRLASE11.

PRINTS; pR009737; GLEYDRLASE16.

PROSITE; pS00776; GLYCOSYL_HYDROL_F11_1; 2.

PROSITE; pS00777; GLYCOSYL_HYDROL_F16; 2.

PROSITE; pS01034; GIYCOSYL_HYDROL_F16; 2.

PROSITE; PS01034; GIYCOSYL_HYDROL_F16; 2.
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             "Novel lichenases from soil.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF254961; AAK50614.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Rodriguez V., Mellado R.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        744 TQDIPKTPGK:IMMNAWPGLTVDDWLKAFN-GRTPLTAHYQWVTYNK
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58; Conser
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                    TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 149
KHTATTQVPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PLYAHYDWVRYTK
                                      RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
                                                                              ESLGKDTTKVQFNYYTNGAG---NHEKLADLGFDAANAYHMYAFDWQPNSIKWYVDGQ-L
                                                                                                                    EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                            TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI
                                                                                                                                                                                                                                                                                                                                                                 PS01034;
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Pred. No. 3.7e-08;
                                                                                                                                                                                                                                           Score 239.5;
Pred. No. 1.1e
24; Mismatches
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1.1e-08;
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01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
Beta-1,3-1,4-glucanase.
Bactlius subtilis.
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van Rensburg P., van Zyl W.H., Pretorius Endry I.S.;
plucanase gene together with the Burly1viprio fibrisolities endo-beta-1,3-1,4-
glucanase gene in Saccharomyces cerevisiae.";
glucanase gene in Sacc
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01-NOV-1996
01-NOV-1996
01-DEC-2001
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Bacteria; Firmicutes;
Bacillaceae; Bacillus.
CBI_TaxID=1423;
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                                                                                          TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPT----DGTPWDEIDI
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25; Mismatches
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Matches 62
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R Pfam; PF00722; Glyco_hydro_16; 1.
R PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYY .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9FDC9;
Q9FDC9;
01-MAR-2001
EXINCI M., Flint H.J.;
EXINCI M., Flint H.J.;
"ISOLation and overexpression of a gene encoding beta-(1,3-1,4)-glucanase from Streptococcus bovis Submitted (MAR-1997) to the EMBL/GenBank/DDBJ dat EMBL; Z92911; CAB07443.1; -.
HSSP; P23904; lAJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-DEC-2001 (TrEMBLrel. 19, Beta-(1,3-1,4)-glucanase pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yao W., Wang Y., Song W., Yang K., Su Z.;
"Gene cloning of an antifugal protein.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
EMBL; AF284449; AAG02415.1;
HSSP; P23904; IAJK.
                                                                                                                                           STRAIN-JB1;
                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                             Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                     Streptococcus bovis
                                                                                                                                                                                                                                                                                                                                                                                                                            007856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endo-1,3-1,4-beta-glucanase (Fragment).
Paenibacillus polymyxa (Bacillus polymyxa).
Bacteria: Firmicutes: Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                NCBI_TaxID=1315;
                                                                                                                                                                                                                                        Streptococcaceae;
                                                                                                                                                                                                                                                                                                             LICHENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                               007856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paenibacillaceae; Paenibacillus.
NCBI_TaxID=1406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 139
                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -VLKHT---ATTNIPKTPGQIMMNLWNGTGVDSWLGPYNGVN-PLYAEYDWV---KYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLTSSAYNK-FDGGEYRSKNTYRYGLYEVNMKPAKNTGIVSSFFTYTGP---ANGTQWDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTINVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHTATNQIPTTPGK--IMMNLWNGTGVDERLGSYNGVN-PLYAHYDWVRYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDIEFLGKDTTKVQFNYYTNGIGGH---EKVVDLGFDASSGFHTYAFDWQPGYIKWYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212
212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                        Streptococcus.
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24127 MW;
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                                                                                                                                                                                                                                                           Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                precursor
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Last annotation updat
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Pred. No. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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es 73;
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                                                                                                                                                                                                                                                           group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                              JBI
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                                                                                              extracellular
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RESULT 13
Q97FD3
ID Q97FD
AC Q97FD
DT 01-OC
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Q93UII
ID Q93UII
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Best Local S
Matches 54
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Best Local :
Q97FD3;
01-OCT-2001
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20, Endo 1-3,1-4-beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                      Q97FD3
                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2000) to the EMBL; AF254960; AAK50613.1;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q93UI1
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                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Rodriguez V., Mellado R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; environmental samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uncultured bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q93UI1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=77133;
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                                                                                                                                                                                                                                                                                                                                                                                                Novel lichenases from soil.";
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                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                   PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKVQFNYYT---SGQGNHEYLYNLGFDASQGFHTYGFDWQADHITWYVDGRAVYTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ
                                                                                                                                                                                                                       TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNNIPSTPGKIMMNAWPGTHEVDSWLGAYN-GRTPLYAYYDWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSNLTGTQG-LRFNLW--SSESAAWVGQFDESKLPLFQFINWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YTGGEWRSKERFGYGLFQVNMKPIKNPGVVSSFFTYTGPS---DGTKWDEIDIEFLGKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP
                                                                                               KHTATTQVPAAPGK---IMMNLWNGTGVDDWLGSYN 197
                                                                                                                       RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFD 176
                                                                                                                                                                        EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                                                                TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE----GTPWDEIDI
                                                                                                                                                 ESLGKDTTKVQFNYYTNGAG - -
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237 ‡
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205 AA;
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                Conservative
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                                      PRELIMINARY,
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237
26989 >
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22890 MW;
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36.1%;
18,
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                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment).
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 Last
              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
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BETA-(1,3-1,4)-GLUCANASE.
TDEF5BCE53790470 CRC64;
                                                                                                                                                                                                                                                            Score 223; DB 2; Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 230;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                      PRT;
                                                                                                                                                                                                                                                                                                 E7CADAAFE02A2F51 CRC64;
                                                                                                                                                -NHEKLADLGFDAANAYHMYAFDWQPNSIKWYVDGQ-L
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 sequence update)
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                                      246
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.2e-08;
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RESULT
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                                                           rne genome c
C58.":
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MEDLINE-21359325; PubMed-11466286;
Moelling J., Breton G., Omelonko M.V., Makarova K.S.,
Noelling J., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf 'Gibson R., Lee H.M., Dubois J., Cinchita Soucaille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium
Clostridiales; Clostridiaceae; Clostridium
Science
[2]
                                                                                                                                     Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., V Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., (Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Pk., Gordon-Kamm B., Liab L., Kim S., Hendrick C., Zhao Z.-Y., De Gordon-Kamm B., Liab L., Kim S., Hendrick C., Zhao Z.-Y., Ochumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, Endo-1,3-1,4-beta-glycanase,
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PRINTS; PR00737; GLYCDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
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"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4323-4838(2001).

EMBL; AE007778; AAX30751.1;
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STRAIN=ATCC 824 /
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MEDLINE=21608550; PubMed=11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha
Rhizobiaceae; Rhizobium.
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58; Conser
                                        294:2317-2323(2001)
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                                                                                                           natural genetic
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Pred. No. 2.
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2.2e-07;
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                                                                                                           Agrobacterium
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Rhizobiaceae
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Dolan M.,
                                                                                                              tumetaciens
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MEDLINE=21608551; PubMed=11743194;
GOOdner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2333-2338(2001).
EMBL, AE008279; AAK89373.1; -.
EMBL, AE008279; AAK89373.1; -.
                                                                                                                                                                                                                 "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium 10ti.";
DNA Res. 7:331-38(2000).
EMBL: AP003006; BAB51743.1;
InterPro: IPR00757; Glyco_hydro_16;
Pfam; PF00722; Glyco_hydro_16; 1.
PFam; PF00723; GLYCO_hydro_16; 1.
PRINTS: PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                                                       Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa K., Kawashima K., Kimura T., Kisokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
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Q98C78;
                                                                                                                                                                          Complete proteome. SEQUENCE 293 AA;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Phyllobacteriaceae; Mesorhizobium.
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    112
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51; Conser
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REFACGEIQTKQRFGYGTYEARLKTDTGSGLNAAFFTYIGPS---DKQPWDEIDFEILTK 168
                        KDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGK 87
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                                                                                    11.0%; Score 200; DB 1
larity 33.8%; Pred. No. 7e-06;
Conservative 27; Mismatches
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EXOK.
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                            EGGQVSNLTGTQGLRFNLWSSES-AAWVGQF 175
                                                               DTSKVQVNAYIDGKGKNEKLVE----VPGGTDKAFNDYAFVWEKDSLRWYVNGQLVNTIT
                                                                                     NPGSFQSN-IITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRK-T 145
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Search completed: July 11, Job time : 34 secs 2003, 10:53:49

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RESULT 2
US-08-103-998-2
; Sequence 2, Application U
; Patent No. 5470725
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequential Codin
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; TYPE: PRT
; ORGANISM: Fibrobacter
US-09-286-690-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 228; Conserv
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US-08-726-320-3
US-09-208-716-1
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Listing

Total number of hits satisfying chosen parameters:

262574 seqs,

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Database

Issued_Patents_AA:*

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Sequence: Title: Perfect score:

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protein search, using sw model

GenCore version Copyright (c) 1993 - 2003

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July 11,

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Scoring table:

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SUMMARIES

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US-09-269-657-3

Sequence

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Sequence

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GENERAL INFORMATION:
APPLICANT: L1, X1n-Llang
APPLICANT: LJungdahl, Lars G.
APPLICANT: LJungdahl, Lars G.
APPLICANT: LJungdahl, Lars G.
TITLE OF INVENTION: L1chenase and Coding Sequences
FILE REFERENCE: 55-96
CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
                                                                                                                                                                                                                        RESULT 3
US-09-286-690-8
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                                                                                                                                                                                      Sequence 8, Application US/09286690 Patent No. 6103511
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 16-OCT-1991
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: A Thermostable (1,3-1,4)-beta-Glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                KHT---ATANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT 237
                                                                                                                                                                                                                                                                                                                                RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                                                                                                                                                                                                                                                                                                                                                                                          EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
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Von Wettstein, Dietrich
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RESULT 5
US-09-286-690-9
; Sequence 9, Application US/09286690
; Patent No. 6103511
; Patent No. 6103511
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US-09-286-690-10
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TYPE: PRT
ORGANISM:
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 242
TYPE: PRT
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Best Local Similarity
Matches 58; Conserv
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Best Local Similarity
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EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/286,690 CURRENT FILING DATE: 1999-04-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Li, Xin-Liang APPLICANT: Ljungdahl, La APPLICANT: Chen, Huizhon
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                                                                                                                    KHTATTQIPQTPGK--IMMNLWNGAGVDEWLGSYN-GVTPLSRSLHWVRYTK 242
                                                                                                                                                   RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                                        EFLGKDTTKVQFNYYTNGVG---NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-L
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Pred. No. 6.9e-15;
Pred. No. 6.9e-15;
                                                                                                                                                                                                                                                                                                                                              Score 233.5; DB 3
Pred. No. 1.5e-13;
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Ljungdahl, Lars G

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US-09-286-690-7
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LENGTH: 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
FILE REFERENCE: 55-96
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CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
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NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                              LENGTH: 238
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                                                                            80 VDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 139
                                                                                                                                                           20 ALTINVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVE 79
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QEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                      IDIEFLGKDTTKVQFNYYTNGVGGH----EKIINLGFDASTSFHTYAFDWQPGYIKWYVDG
                                                                                                                     SLTSPANNK-FDCGEYRSTNNYGYGLYEVSMKPAKNTGIVSSFFTYTGPSH---GTQWDE 129
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                                                                                                                                                                                                Score 227.5; DB 3; Pred. No. 5e-13;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-286-690-11
                                                                                                                                                                                                                                                                                                                                                            Sequence 4,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/286,690 CURRENT FILING DATE: 1999-04-05 EARLIER APPLICATION NUMBER: US 60/027,882 EARLIER FILING DATE: 1999-10-04 EARLIER APPLICATION NUMBER: PCT/US97/1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chen, Hui
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1997-10-03 NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                               ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                 TITLE OF INVENTION: A Thermostable (1,3-1,4)-beta-Glucanase NUMBER OF SEQUENCES: 4
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                      APPLICANT:
               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                           CITY: Alexandria
                                                                                                                                                           ADDRESSEE: FOLEY & LARDNER STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 SKLPL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 DFHTYGFEWRPDYIDFYYDGKKYYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 AFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 VSTVLEAFTGDISNGKMILTLDREYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 VAAAAAALTINVS-----AKDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242
                                                                                                                                                                                                                                                                                                                                                                 5470725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSFFTYTGFS---DNNPWDEIDIEFLGKDTTKVQFNWYKNGVGG---NEYLHNLGFDASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSMFLYQNCSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -VLKHT---ANTINIPSTPGKIMMNLWNGTGVDSWLGSYNGAN-PLYAEYDWV---KYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ljungdahl, Lars G.
                                                                                                                                                                                                                                                                                                                                                                                Application US/08103998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, Xin-Liang
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                                                                                                                                                                                                                                                    Von Wettstein, Dietrich
                                                                                                                                                                                                                                                                      Thomsen, Karl Kristian
Olsen, Ole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                         Borriss, Rainer
                                                                                                                                                                                                                                                                                                          Hofemeister, Jurgen
Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lichenase and Coding Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 224.5; DB 3;
Pred. No. 9.5e-13;
5; Mismatches 71;
Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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117

PRIOR APPLICATION DATA:

CLASSIFICATION: 435 FILING DATE: APPLICATION NUMBER:

APPLICATION NUMBER: US 07/773,652 FILING DATE: 16-OCT-1991

CURRENT APPLICATION DATA:

US/08/103,998

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US-09-286-690-2
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                                                                                                                      Matches
                                                                                                                                 Best Local Similarity
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 2, Application US/09286690 Patent No. 6103511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Lichenase and Coding FILE REFERENCE: 55-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: L1, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEPAX: (703) 683-4109
TELEFAX: 8001/6
                                                                                                                                                                                                                                                      LENGTH: 245
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ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 EFLGKDTTKVQFNYYTNGAG---NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L 187
  81
                                          79
                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 TSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 INVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
DIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQ 140
                                    LTIDRDGSGYTCGEYRTKNYYGYGMFQVNMKPIKNPGVVSSFFTYTGPS---DGTKWDEI
                                                                        LTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KHTATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYDWMRYRK 236
                                                                                                                10.4%; Score 190.5; ilarity 31.6%; Pred. No. 1.2c Conservative 17; Mismatches
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                                                                                                                1.2e-09;
.ches 87;
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                                                                                                                                                     DB 3;
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                                                                                                                                                       Length 245;
                                                                                                                  Indels
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US-08-824-707-2
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                                                                                                                                                                                                                                                                                   Query Match 8.7%; Score 159.5; DB 2; Best Local Similarity 27.6%; Pred. No. 1.1e-06; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:

ZIP: 10174-64U1
ZIP: 10174-64U1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
COMPUTER: TOTAL Release #1.0, Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPUTER:

OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: PATENTIA Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6
FILING DATE: 14-April-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35, 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: 306 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 405 L...
STREET: New York
CITY: New York
STATE: New York
OCHUTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENIES: 4
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ANDRESSEE: No. 59196880 No. 5919688disk of No.
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 212-867-0123
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
 262
                               172 VGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDF 205
                                                                        220
                                                                                                        112 AVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAW 171
                                                                                                                                             163
                                                                                                                                                                                                                  103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 AVYTA----YDNIPDTPGKIMMNAWNGIGVDDWLRPFN-GRTNISAYYDWV 238
                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2,
                                                                                                                                                                                                                                  2 NIKKTAVKSALAVAAAAALTTNVSAKDESGAELYTLEEV--QYGKFEARMKMAAASGTV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Application US/08824707 5919688
V--FDQ---PEFLILN-VAIGGQWPGNPDATTPF 289
                                                                    GWSFADD--FHTFGIDWTPGEITWLVDGQEYHRVTTADVG--
                                                                                                                                       SAFWMV--GANLPD-TPWPTSGEIDIMENVGNAPHEVHGTVHGPGYSGDNGIMGTYQHPQ 219
                                                                                                                                                                           SSMFLYQNGSEIADGRPWV---EVDI-EVLGKNP----GSFQSNIITGKAGAQKTSEKHH 111
                                                                                                                                                                                                                  NYTTSRVNSALDGQGNLVITALQESDGSYTSARLTTQGNVQPQFGRIEARIQIPRGQGIW 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asenjo, Jun...
Asenjo, Jun...
Cavva, Demitris
                                                                                                                                                                                                                                                                                                                                                                                                                                  306 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halkier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hedegaard, Lisbeth
Halkier, Torben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferrer,
                                                                                                                                                                                                                                                                                                                                                                                                  linear
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14-April-1997

ON: 435
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                                                                                                                                                                                                                                                                                                                      Length 306;
                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                     Gaps
                                                                      - ANOW
                                                                      261
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CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER APPLICATION NUMBER: 0885/96
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1997-04-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 11
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US-09-159-106-2
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Best Local
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LENGTH: 263
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Patent No. 6284509
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CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0.27/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0.885/96
EARLIER APPLICATION NUMBER: 0.85/96
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1997-04-14
                                                                                                                                                                                                                                                         TITLE OF INVENTION: An Enzyme With TITLE OF INVENTION: Activity FILE REFERENCE: 4693.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: An Enzyme With -1,3-Glucanase TITLE OF INVENTION: Activity FILE REFERENCE: 4693.204-US
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APPLICANT: Diers, Ivan
APPLICANT: Halkier, Torben
APPLICANT: Hedegaard, Lisbeth
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TYPE: PRT
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SOFTWARE: FastSEQ for
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APPLICANT: Diers, Ivan
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APPLICANT: Hedegaard, Lisbeth
LENGTH: 435
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US-09-159-106-11
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SEQ ID NO 13
LENGTH: 303
TYPE: PRT
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                                                                                                                                                                    Query Match
Best Local
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EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1997-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: An Enzyme With -1,3-Glucanase TITLE OF INVENTION: Activity FILE REFERENCE: 4693.204-US CURRENT APPLICATION NUMBER: US/09/159,106 CURRENT FILING DATE: 1998-09-23
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ
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APPLICANT: Diers, Ivan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 MYQHPQGWSFADTFHTFAVDWKPGEITWFVDGQQFHRVTRASVG------ANAWVFD
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                                      34 ---ELYTLE-----
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78; Conserv
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AELQNYTASFANSALDGQGNLVITARREGDGSYTSARMTTQGKYQPQYGRIEARIQIPRG
                                                                       :|: :|| ||| || |: || |: :| :| :| || SALVAALTAAAAALAVTYAATSAAAAPGDLLWSDEFDGAAGSAPNPAVWNHETGAHGWGN
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                                                                                                                                           34; Mismatches
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                                                                                                                                                                  Score 141.5;
Pred. No. 4.
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Pred. No. 4.9e-05,
                                                                                                                                                                    4.9e-05;
                                                                                                                                                                                     DB 4;
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                                    ---EVQYGKFEARMKMAAA
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US-08-712-072C-4
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                                                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO: .
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                 FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Elizabeth A.
REGISTRATION NUMBER: 39,911
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                                                                                                                        / Match 7.3%;
Local Similarity 23.7%;
les 44; Conservative 3
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                            83 -EVLGKNP----GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTV 137
                                                             93
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                                                                                     28 KDFSGAELYTLEEVQ--YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV---EVDI 82
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MEHVGENPDVVHGTVHTKAYNHLLGTQRGGSIR---VPTARTDFHVYAIEWTPEEIRWFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGS----DFTLDWTDNFDTFDGS
                                                          REYTSARLYTRGKASWTYGRFEIRARLPSGRGTWPAIWMLPDRQTYGSAY-WPDNGEIDI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANAWV--FDQ---PFFLILN-VAVGGQWPGYPDGTTQLPQQMKVDYVRVYDNGSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QG-IWPAFWMLGGS--FPGTPWPSSGEIDIMENVGFEPHRVHGTVHGPGYSGGSGI--TG 202
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                                                                                                                                                                                                                                                                                                                                                                                                    (212) 286-0854 or 286-0082
                                                                                                                                                                                                 gub, Rhodothermus marinus
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/ENTION: ENDO-BETA-GALACTOSIDASE
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                                                                                                                                     Score 133.5; DB:
Pred. No. 0.00023
                                                                                                                        Mismatches
                                                                                                                                                   DB 2;
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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: e13b
US-08-712-072C-3
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US-08-712-072C-3
                                                                                                                                                                                             Matches
                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 286-0854
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL: I
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bogosian, Elizabeth A. REGISTRATION NUMBER: 39,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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128 WTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESA----
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                                                  184 GTWAASGEIDVMEARGRLPGSVSGTIHFGGQWPVNQSSGGDYHFPEGQTFANDYHVYSVV 243
                                                                                                                         124
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                                                                                                                                                      20 ALTTNVSAKD-----FSGAELYTLEE--VQYGKFEARMKMAAASGTVSSMFLYQNGSEI 71
                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                      AMNDSKSPQDPNRYAQYSSGKINTKDKLSLKYGRVDFRAKLPTGDGVWPALWMLPKDSVY 183
                                                                                   ADGRPWVEVDI-EVLGKNPGSFQSNIITG---KAGAQKTSEKHHAVSPAADQAFHTYGLE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRVYRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                           321 amino acids
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                                                                                                                                                                                             Conservative
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N: 435
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ENDO-BETA-GALACTOSIDASE
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                                                                                                                                                                                           34; Mismatches
                                                                                                                                                                                                         Score 119; DB 2
Pred. No. 0.006;
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                                                                                                                                                                                           84; Indels
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                                                                                                                                                                                                                           Length 321;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Run
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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length: 2000000000
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Match Length
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/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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US-10-156-761-13203
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10 US-09-845-272-2
10 US-09-815-242-13423
10 US-10-156-761-11953
US-10-156-761-10925
US-10-156-761-9303
                                                                                                                                                                                                                               US-10-156-761-14970
US-09-734-569-152
US-10-156-761-9339
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 US-09-841-132-444
US-09-801-368-362
US-09-841-132-195
                                            US-09-738-363-2
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                                     Sequence 152, App
Sequence 9,39, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 13203, A
Sequence 1323, A
Sequence 13423, A
Sequence 11953, A
Sequence 10925, A
Sequence 10925, A
Sequence 9303, A
Sequence 9303, A
Sequence 9, Appli
Sequence 9, Appli
                                                                                                                                                                                                                                                                                        Description
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Sequence 152, Ap
  Sequence
              Sequence
                            Sequence
e 444, App
e 362, App
e 195, App
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89	89	89	89	89	89	89.5	89.5	89.5	90	90	91	91	91	91	91.5	92	92	92.5	93	93	93.5	95	95	95.5	96
4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.1	5.1	5.1	5.1	5.2	5.2	5.2	5.3
499	499	499	499	499	499	1236	1162	493	1281	674	1751	1751	678	279	701	839	777	377	714	156	450	462	400	1289	1776
									9	9	10	10	10	9	9	9	9	9	9	10	9	9	9	10	10
US-10-175-752-592	US-10-175-738-592	US-10-173-706-592	US-10-175-737-592	US-10-176-758-592	US-10-174-590-592	US-09-769-787-109	US-09-745-008-34	US-09-738-626-6780	US-10-156-761-9789	US-10-086-464-14	US-09-841-132-594	US-09-841-132-445	US-09-801-368-314	US-09-738-626-3942	US-10-156-761-12041	US-10-231-035-6	US-10-156-761-10762	US-10-149-819-7	US-09-738-626-6377	US-09-925-301-1154	US-10-156-761-14443	US-09-903-185-13	US-09-903-185-2	US-09-738-363-4	US-09-841-132-179
	592,		Sequence 592, App	592,	•	Sequence 109, App	Sequence 34, Appl	Sequence 6780, Ap	Sequence 9789, Ap	Sequence 14, Appl	Sequence 594, App	Sequence 445, App	Sequence 314, App	Sequence 3942, Ap	Sequence 12041, A	Sequence 6, Appli	Sequence 10762, A	Sequence 7, Appli	Sequence 6377, Ap	Sequence 1154, Ap	Sequence 14443, A	Sequence 13, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 179, App

ALIGNMENTS

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US-10-156-761-14970
                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Streptomyces avermitilis US-10-156-761-14970
                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 14970
LENGTH: 420
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14970, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION HUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: HOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 2001-204089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OMURA, SATOSHI
                                        135 WTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKY 194
                                                                                  173 VMENVGFEPSTIHGTIHGPGYSGTGGIGAAYSLPGGQAFA----DAFHTFAVDWAPDSIT 228
                                                                                                                                                                       125 NTSGK-FSAA-----YGRVEARMKIPRGQGMWPAFWML--GTDIGQVGWPNSGEID
229 WSVDGTVYQRRTPADLGGKT------WA-----FNK---PFFLILN-LAVGGY
                                                                                                             82 I-EVLGKNPGSFQSNII-----TGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVR 134
                                                                                                                                                                                                        24 NVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIAD-GRP-WVEVD
                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                              6.7%;
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                                                                                                                                                                                                                                                       Score 122.5; DB 9;
Pred. No. 0.032;
8; Mismatches 66;
                                                                                                                                                                                                                                                                                                  Length 420;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                            47;
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RESULT 3
US-10-156-761-9339
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                                            APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                         Sequence 9339, Application US/10156761 Publication No. US20030119018A1
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 181
SOFTWARE: PATENTIN VET. 2.1/WC
SEQ ID NO 152
LENGTH: 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                              TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: In the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24
                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICANT: Renz, i
APPLICANT: Ehrhar
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                                                                                                                                                                                                                                                                                                                                                               175
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     APPLICATION
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US20020064816A1
                                                                                                                                                                                                                                                                                                                            LDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKN 239
                                                                                                                                                                                                                                                                                                                                                                                                                             VDGVGGRE-QQMYLGFDPSAD--FHYYRFRWSKDMVVFYVDNKPVR----VFKNLEGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGT- 156
                                                                                                                                                                                                                                                                                                                                                            PGTKYLNQQAMGVYISIWDGSSWATQG----GRVP----
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Schmidt, Ralf-Michael
Reski, Ralf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cirpus, Petra
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NUMBER: US/10/156,761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 120; DB 10; 23.0%; Pred. No. 0.031; 70. Mismatches 70;
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US-09-988-200-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09988200 Patent No. US20020094553A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9339
LENGTH: 629
TYPE: PRT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/269,731
FILING DATE: <UNKnown>
APPLICATION NUMBER: FR 96 12204
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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47; Conserv
                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTSVDKVAAGGVQAEVDWVRV 625
                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                          STATE: VIRGINIA
REGISTRATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLOAREG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HENRISSAT, Bernard
YVIN, Jean-Claude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RICHARD, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTIN, Philippe
                                                                                                                                                                                                                                                                                                                                                          Highway
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23.4%;
NUMBER: <Unknown>
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ
STREET: 612 Crystal Square 4, 1745 Jefferson Davis
                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    545 TTMRFTVDDRLVQETTRNKLESTRGQWVYDHNQYVILNLALGGAYPAGWNQVTSPYWGLP 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 NYVRWTVDGQEVRKTEGGQVSNLTG-----TQGLRFNL------WSSESAAWVG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488 ---PASGETDIMENIGYSDWTSSALHGPGYSADGNIGARQTYPGGGTADHWHTYAVEWTP 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 DFTSGRVDTNTRFDFTYGRVSARMKLPVGDGFWPAFWLL--GSNVDDPSVSW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAAD------QAFHTYGLEWTP 130
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APPLICATION NUMBER: US/09/988,200 FILING DATE: 19-NO. US20020094553A1-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \begin{tabular}{ll} \textbf{INVENTION:} & \textbf{Glycolyse} & \textbf{hydrolase} & \textbf{genes} & \textbf{and} & \textbf{their} \\ \textbf{use} & \textbf{for} & \textbf{producing} & \textbf{enzymes} & \textbf{for} & \textbf{the biodegradation} \\ \end{tabular}
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Pred. No. 0.14;
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; TOPOLOGY: linear;; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-988-200-6
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US-10-294-561-3
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Publication No. US20030096329A1
GENERAL INFORMATION:
APPLICANT: Seikagaku Corporation
                                                                                                                                                                                                                                                                   Query Match 6.4%;
Best Local Similarity 22.3%;
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
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CURRENT FILLING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: JP 2001-351943
PRIOR FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: (1-3)-Beta-D-Glucan Binding Domain Protein, Measuring Method Usi
TITLE OF INVENTION: Substance And Assay Kit
FILE REFERENCE: Q72918
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 673
TYPE: PRT
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INFORMATION FOR SEQ ID NO:
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                    174
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                                                                                                                                                                                                                 LTTNVSAKDFSGAELYTLEEV-----QYGKFEARMKMAAASGTVSSMFLYQNGSEIA 72
                   QFD--ESKLPLFQFINWVKVYKYTPGQGEGG--
                                                                                   -FHTYGLEWTPNYVRWTVDGQEV--RKTEGGQVSNLTGTQGLRFNLWSSESAA----WVG 173
                                                                                                                   ----WMSGDNTNYVRWPSSGEIDFIEHRNTNNEKVRGTIHWSTPDGAHAHHNRESNTNGI 176
                                                                                                                                                 DGRPWVEVDIEVLGKNPGSFQSNIITGK-AGAQKTSEKHHAVSPAADQA------
                                                                                                                                                                                    LVITAKREDYDGFK-YTSARLKTQFDKSWKYGKIEAKMAIPSFRG-VWVMF------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WTVDGQEVRKTEG----GQVSNLTGTQGLR--FNLWSSE----SAAWVGQFDESKLPLFQF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HNIVVKNGKPTWMRPGSFPQTNHNG-----YHLPFDPRND--FHTYGVNVTKDKIT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EVLGKN-----PGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVELTQKSAVRESDHDL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGKFEARMKMAAASGTVSSMF-LYQ--NGSEIADGR-PWVEVDI-------
                                                  DYHIYSVEWNSSIVKWFVNGNQYFEVKIQGG----VNGKSAFRNKVFVILNMAIGGNWPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WYVDGEIVGEKDNLYWHRQMNLTLSQGLRAPHTQWKCNQFYPSANKSAEGFPTSMEVDYV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 412-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                 Score 116.5; D) Pred. No. 0.19;
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Pred. No. 0.
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                 -SDFTLDWTDNFDTFD
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US-09-988-200-8
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Best Local :
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 103
                                  142
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 ---AQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEG---GQVSNLTGT 156
                                WLYSDFDYSVANGETVYSEIDVVELQQFDWYEGHQDDIYDMDLNLHAVVKENGQGVWKRP
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Sequence 8, Application US/09988200 Patent No. US20020094553A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,200
ETLING DATE: 19-NO. US20020094553A1-2001
CLASSIFICATION: - (Unknown)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYFE: Floppy disk
                                                                                                                                                                                                                MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 412-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: IRA SCHULTZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 -FDVADEAFPAKMYIDYVRVYQDASTSSPVGDTSLDGYYFVQNRHSELYLDVTDASNE-D
63 FLYON-GSEIADGRP-WVEVDIEVL----
                                       82 VKISNGIAELTMRHNANNTPPDGGTYFTSGIFKSYQKFTYGYFEAKIQGADIGEGYCPSF 141
                                                                            8 VKSALAVAAAAALTTNVSAKD----FSGAELYTLEEVQYGKFEARMKMA-AASGTVSSM 62
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAFLQQ - - WST SGNENQQFDFEHLENNVY
                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: <Unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FR 96 12204 FILING DATE: 07-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/269,731 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ STREET: 612 Crystal Square 4, 1745 Jefferson Davis
                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF INVENTION: Glycolyse hydrolase genes use for producing enzymes
                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVIN, Jean-Claude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RICHARD, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTIN, Philippe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Highway
                                                                                                                                                                                                                                                                                                                                                           (703) 412-1161
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                                                                                                                     61;
                                                                                                                                  Score 114.5; D
Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                       <Unknown>
                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    <Unknown>
-GKNPGSFQSNI----ITGKAG-----
                                                                                                                                                          DB 10;
                                                                                                                   131;
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102
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APPLICANT: DECKER, STEPHEN R.

APPLICANT: HIMMEL, MICHAEL E.

TITLE OF INVENTION: THERMAL TOLERANT MANNANASE FROM ACIDOTHERMUS

TILE OF INVENTION: CELLULOLYTICUS

FILE REFERENCE: 40197.7US01

CURRENT APPLICATION NUMBER: US/09/917,378

CURRENT FILING DATE: 2001-07-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 1

LENGTH: 7.7
                                                                                                                                                                                                                          US-10-156-761-13203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : LENGTH: 762
; TYPE: PRT
; ORGANISM: Acidothermus cellulolyticus
US-09-917-378-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-917-378-1
                                       APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
APPLICANT: SAKAKI, YOSHIYU
                                                                                                                                                               Sequence 13203, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09917378 Publication No. US20030119093A1
                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 FNLWSSESAAWVGQFDE-----SKLPLFQFINWVKVYKYTPGQ------
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        INVENTION:
                                       ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                       ALAISTGTSPPPSPSSSSPSSSPSPSPSPSASPSASSSPSPSPSSSSPVSGGV 459
                                                                                                                                                                                                                                                                                                                                                                                                                        -GEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNIYSRDGMLILALTRKGQE 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTSEKHHAVSPAADQAFH---TYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLT-GTQGLR 160
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                                                                                                                                                                                                                                                                                                                                          SFNGQVPRDDEPAPQSS-SSAPASSSSVPASSSSVPASSSSAFVPPSSSSATNAI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSV-----NNASIAQIVTLKANTSYKVSAFGKASSPGTSAYLGISKASN
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                                                                                                                                                                                                                                                                                                                                                                                   NGEAG-----W--NEWMLAGNVNGQPYPNYDGFNV-----YYPSSTATVLA-----SE
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    NOVEL POLY
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26.0%; Pred. No. 0.1
      POLYNUCLEOTIDES
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Q
                                                                                                                   ; TYPE: PRT ; ORGANISM: Chlamydia trachomatis US-09-841-132-353
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                                       Query Match
Best Local S
Matches 89
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Best Local S
Matches 76
                                                                                                                                                                             SOFTWARE: FastSEQ for
SEQ ID NO 353
LENGTH: 583
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 353, Application US/09841132 Patent No. US20020061848A1
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SEQ ID NO 13203
LENGTH: 363
TYPE: PRT
                                                                                                                                                                                                                                   APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bhatia, Ajay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 --TYLRGYRTT-----GDDGTVEFTTIFPGWYPPRAPHIHVKVHTGGTSTDRTYQG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 GLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKLPLFQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103
                                         89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 ALAVAAAAALTTNVSA-KDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 EIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKT----SEKHHAVSPAADQAFHTY 124
8
                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTTP 318
VKSALAVAAAAALTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGFTGTLTVAVDPEEEGRGADTVGAGSPPPGGA---PSGSPSTGTPSGPSPTATPTVTPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESFNGQVPRDDEPAPQSSSSAPASSSSVPASSSSVPASSSSAFVP--PSSSSATNAIHGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKVNWTGQLFFDDRYGDEVYGTSPYTEHTGTRTRLTEDTVYAGGGARDG--LMAVTGDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FINWVKVYKYTPGQGEGGSDFTLDWTDNFD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCDAAGHYSGYPTAGP--AGTAPGPAGGSTDTSGA---------DER-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALGGAAAGAAMGLGISSCSSDSGAR--TSGSPAHGASGTDVCVLNSSATEGSYYL----
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349
                                                                                                                                                                                                                      Windows Version 3.0/4.0
                                                         5.9%;
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                                       51;
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                                   Score 108; DB 10;
Pred. No. 0.82;
1; Mismatches 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 109; DB Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                       INFECTION
                                                                                                                                                                                                                                                                                                                                          FOR TREATMENT
                                     174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9:
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                                                                          Length 583;
                                       Indels
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                                       84;
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                                     Gaps
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SEQUENCE
US-09-765-272-2
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US-09-765-272-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09765272 Patent No. US20020061545A1
    Query Match
                                                                                                                                                                                TELEFAX: (301) 309-8 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version
                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAVAKEHRNLVNA------KGAKVNPNGHKRYRVN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTPESSTPSSSSPASTPEVVASAKINRFFASTAEPAAPS---LTEAESDQTDQTETSDTN 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GDWTFDGNRVDLTDK-----NIYSRDGMLILALTRKGQESFNG------QVPRD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYPSHWRP-----LDTQVSESPESTPSPDDVLGKGGGIYTEKSLTITGITGTIDFVSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYGLEWTPNYVRWTVDGQEVRKTE------GG------QVSNLTGTQGLRFNL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDIDVSIENILNVAINQNTSAKKGGAIYGKKAKLSRIN 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEPAPOS-SSSAPASSSSVPAS------SSSVPASSSSAFVPPSSSSATNAIHGMRTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVGEVIFSEN----TAKGHGGGICTNKLSLSNLKTVTLTKNSAKESGGAIFTDLASIPTT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTLDWTDNFDTFDGSRWGK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGPPAE--FC 138
                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/961,083 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -ATDSGA--GVFTKENLSCTN-TNSLQFLKNSAGQHGGGAYVTQTMSVTNTTSESITTPP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSEI--ADGRP---WVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Maryland
                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                         NAME: Brookes,
                                                                                                                                                             LENGTH: 666 amino acids
                                                              DESCRIPTION:
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    5.98;
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                                                              SEQ ID
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    Score 107.5;
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Length 666;
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Ş
                                                                                                                      ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13423
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                                                                                                                                                                                                     SEQ ID NO 13423
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                                       Matches
                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 76; Conserva
                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-05.27
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                     SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                           PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                            Local
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 6
FILING DATE: 2000-11-
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          517 NHIKTSQFVAFDELFAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGS 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 QKTSEKHHAVS----PAADQAFHTYGLEWTPNYVRWTV--DGQEVRKTEGGQVSNLTGTQG 158
57 GTVSSMFLYQNGSEIADGRPWVEVDIEVLGKN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 GTVSSMFLYQNGSEIADGRPWVEVDIEVLGKN-------PGSFQSNIITGKAGA 103
                                       76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRFNLWSSESAAWVGQFDESKLPLF-----QFINWVKVYKYTPGQGE-GGSDFTLDWTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPEDWNIPEGLYRNGEFVFKNGARSTWNSPAPQQPPSTESSSSSSSSSSSSTSQSSSTTPSTN 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSAFVPPSSSSATNAIHGMRTTP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NF-----DTFDG--SRWGKGDWTFDGNRV-----DLTDKNIYSRDGMLILA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSTTTNPNNNTQQS----NTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind, Judith W. Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto, Robert T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                       Conservative
                                                                                                                                                                                                                     for Windows Version 4.0
                                                                                                                                                                                                                                                           2001-02-16
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                                                          5.8%;
23.5%;
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                                                            Score 106.5;
Pred. No. 1.
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                                       Mismatches
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                                                                            DB 10;
                                       105;
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                                                                            Length
  ---PGSFQSNIITGKAGA 103
                                                                              719;
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US-10-156-761-11953
: Sequence 11953, Application US/10156761
: Publication No. US20030119018A1
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION UMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11953
LENGTH: 698
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                    --VDLTDKNIYS--
                                                                                                                                                            YVRWTVDGQEVRKTEGG-----QVSNLTGTQGLRFNLW-----SSESAAWVGQFDES
                                                 -----SWYDPDVHVFKPGVSTPVRQYDLPNTGTSSGADTLAGSGLA---WSPDGSRL
                                                                                      KLPLFQFINWV--KVYKYTPGQGEGGSDFTLDWT---DNFDTFDGSRWGKGDWTFDGNR- 232
                                                                                                                                                                                                PILGSSAGAPGTLVAGAPGQSPVVLGVYDVSSGTATLTAHAFDPGNTGGGNLSDLAVTP-
                                                                                                                                                                                                                                 EVLGKN---PGSF-----QSNIITG--KAGAQKTSEKHHAVSPAADQAFHTYGLEWTPN 131
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HORIKAWA, HIROSHI
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                  -----RDGMLILA---LTRKGQESFNGQVPRDDEPAPQSSSSA
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Pred. No. 1
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US-10-156-761-9706
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9706
LENGTH: 311
TYPE: PRT
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APPLICANT:
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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Local Similarity 22.3%;
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                                                                      AVVLAAGAVVSLRRRRR 311
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                                                                                                     -LVNAKGAKVNPNGHKR
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HORIKAWA, HIROSHI
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Pred. No. 1;
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FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9303
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US-10-156-761-9303
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MĀSĀHIRĀ
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT TILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSI
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LENGTH: 904
TYPE: PRT
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Publication No. US20030119018A1
GENERAL INFORMATION:
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                                                                                                                                                                                                           APPLICANT: SHTBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 21.5%; as 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 SDSASATATATSTATTTAPTAPASTVARPSIVSRT 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 ----LARTTTEAFSIVGVSWTG--AARELDGTAQVRTRGTDTGEWSGWRNLAPGLPVDRT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 MAAASGTVSSMFLYQNG----SEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---RFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGG--SDFTLDWTDNFD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSAPASSSSVPASSSSVPASSSSAFVPPSSSSAT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFDGSRWGKG-DWTFDGNRVDLTDKNIYSRDGMLILALTRKGQESFNGQVPRDDEPAPQS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAGGAGVVTYAVASPSGDAADDVARGKRPVEVHDLAL------KAGTSGSRE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTEAR-NKGLDTSGTGTGLSNAAFVAKDPSQTPTGTPSGSATETGSEP---APAPGD 234
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HORIKAWA, HIROSHI
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US20030119018A1
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Pred. No. 4.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 904;
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Best Local Similarity
Thes 72; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Stre
US-10-156-761-9303
Search completed: July 1.1, Job time : 55 secs
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                                                                  414 VGSFSVAGTGGWQSWRTVPANISS 437
                                                                                                                                                                        223
                                                                                                                                                                                                                                           184 QFINWVKVYKYTPGQG-----EGGSD-FTLDWTDNFDTFDGS------RWG
                                                                                                                                                                                                                                                                                                                134 RWTVDGQEVRKTEGGQV-----SNLTGTQG----LRFNLWSSESAAWVGQFDESKLPLF- 183
                                                                                                                                                                                                                                                                                                                                                202 --- CGTNPGG-PCNETSGIGGN------TPCAGTTCQASFHTYAMEWDRSTSTEEI 247
                                                                                                                                                                                                                                                                                                                                                                                                                     142 RVESRIQLPNVTGAAAKGYWPAFWMLGAPYRGNYQNWPSVGELDIMENVQGLNTDWATVH
                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 KFEARMKM-----AAASGTVSSMFL-----YQNGSEIAD------GRPWVEVD 81
                                                                                                                                                                                                          MVVDYVQVLQSSGGSGTTPPPSGSRDAYSAIQAESYDSQSGTSTETTTDTGGGQNIGSLG
                                                                                                                                                                                                                                                                                                                                                                                 IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAA----DQAFHTYGLEW----TPNYV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces avermitilis
                                                                                                   ASSSSVPASSS----SVPASSSS 297
                                                                                                                                     NGDWALYKG -- VDFGSTAAKQFYAR -----
                                                                                                                                                                        KGDWT-FDGNRVDL---TDKNIYSRDGMLILALTRKGQESFNGQVPRDDEPAPQSSSSAP
                                                                                                                                                                                                                                                                               RFYLDGVNFHTVKASQVDATTWANATG-HGFFVILNVAMGGGFPAAFGGGPDSGTDPGHP 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.5%;
                2003, 11:02:51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100.5; | Pred. No. 2.6;
                                                                                                                                       -VASGAAAGVSGLV----EVRLDSRTGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Database :
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            July 11, 2003, 10:54:20; Search time 71 Seconds (without alignments) 654.992 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          908470 seqs, 133250620 residues
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SIDS2/gcgdata/geneseq/geneseqp-emb1/AA198.DAT:*

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(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_101002:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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Pred. No. is the number of results predicted by chance to he score greater than or equal to the score of the result being and is derived by analysis of the total score distribution. to have a being printed,

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10	10	10	10	10	10	10	10	10	11	Score
2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	3.2	Query Match
387	384	333	322	319	268	209	144	88	361	Length DB
21	21	21	21	21	21	21	21	23	22	BB
AAG49848	AAG19453	AAG49853	AAG49849	AAG19454	AAG49854	AAG45465	AAG45466	ABP03676	ABG25391	ID
Arabidopsis thalia		•	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia		Arabidopsis thalia	Human ORFX protein	Novel human diagno	Description

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Synthetic antifree	AAR08081	11	52	2.3	00	45
hetic antif	AAR08078	11	51	2.3	80	44
uman alpha 2 C	AAW03591	17	50		8	43
ic antif	9	11	46		8	42
ynthetic anti	AAY24058	20	43		80	41
ant	AAR08097	11	41		8	40
ynthetic ant	8	11	41		80	39
ic an	AAR08082	11	41		8	38
netic ant	AAR08080	11	41	2.3	8	37
Synthetic ant	AAR08077	11	40			36
P. americanus	AAY25427	20	38		8	35
Melting pt. depr	AAR14375	12	38		80	34
Winter flound	AAY44713	21	37		80	υ W
P. americanus	AAW86156	20	37		80	32
P. americanus anti	AAW86158	20	37		00	31
P. amer	AAW86157	20	37			30
Protein derived	AAY23880	20	37		8	29
Protein	AAY23879	20	37		80	28
Antifreeze prot	AAR26105	13	37		80	27
Arctic fish an	AAW27490	18	ω		80	26
Human peptide	ABG41399	23	20		8	25
Peptide #59	AAM31884	22	20		8	24
Human bone ma	AAM71587	22	20		80	23
Human brain ex	AAM59054	22	20		8	22
Protein #5609	ABB23610	22	20		8	21
Peptide #5949 enc	ABB38443	22	20		8	20
Arabidopsis	AAG83928	22	10	•	8	19
Arabidopsis thali	AAG83926	22	10	٠	8	18
Arabidopsi	AAG83648	22	10		8	17
Human polype	AAM40232	22	1475		9	16
Drosophila melanc	ABB63936	22	1307		9	15
Drosophila melanc	ABB69366	22	1068	٠	9	14
	AAB99727	22	350		9	13
	238	22	337		9	12
Drosophila melanog	24	22	337		9	11

ALIGNMENTS

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RESULT 1
ABG25391
WPI; 2001-639362/73.
N-PSDB; AAS89578.
                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forension food supplement; medical imaging; diagnostic; genetic disorder
                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                Drmanac RT, Liu C,
                                                                                                              30-MAR-2001; 2001WO-US08631
                                                                                                                                11-OCT-2001.
                                                                                                                                                 WO200175067-A2
                                                                                                                                                                                                             Novel human diagnostic protein #25382
                                                                                                                                                                                                                             18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                  ABG25391;
                                                                                                                                                                                                                                                                 ABG25391 standard; Protein; 361 AA.
                                                                   (HYSE-) HYSEQ INC.
                                                Tang YT
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations

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RESULT 2
ABP03676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical company of sites expressing (II). (I) and (II) are useful for treating company of sites expressing (II). (I) and (II) are useful for treating company of sites expressing (II). (I) and (II) are useful for treating company of sites expressing (II). (I) and (II) are useful for treating company of sites expressing (II). (I) and (II) are useful for treating company of sites expressing (II) and (II) are useful for treating company of the polypeptide and polynucleotide sequences have applications in CC diagnostics, forensites, gene mapping, identification of mutations company to the produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human company to the invention.

CC Note: The sequence data for this patent did not appear in the printed company to the invention of the invention 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                       Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthitis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
                               Shimkets RA,
                                                                                         30-MAY-2000;
29-AUG-2000;
                                                                                                                                       29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                       06-DEC-2001.
                                                                                                                                                                                                    WO200192523-A2
                                                                                                                                                                                                                                                                 myasthenia
                                                                                                                                                                                                                                                                                            hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX protein sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP03676 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 SSSSAPASSSS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
11; Conserv
                                                            CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSSAPASSSS
                                                                                                                                                                                                                                                               gravis.
                                                                                                                                                                                                                                                                              disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                         2000US-206132P.
2000US-228716P.
                               Leach MD;
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                                                                                                                                                                                                                                                                              rheumatoid
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                      ID NO:7334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotide (I) and suseful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
0.092;
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25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 29-MAR-1999;

99US-0121825. 99US-0123180. 99US-0123548. 99US-0125788. 99US-0126264. 99US-0126785. 06-SEP-2000

EP1033405-A2

25-FEB-2000;

2000EP-0301439

Arabidopsis thaliana

termination sequence

Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;

pathway; promoter; Arabidopsis thaliana protein fragment SEQ ID NO:

57085

18-OCT-2000

(first entry)

AAG45466 standard; Protein; 144 AA.

SSSVPASSSS

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 or In the specification). ABN15762 to ABN27552 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated of the contract of a medicament for treating a pathology associated disorder. ORFX-associated of the contract 
                                                                                                          Matches
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Best Local :
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protection or regeneration and treatment of lung or liver fibrosis,
reperfusion injury in various tissues and conditions resulting from
systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.B. The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                          Sequence
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99US-0137724 99US-013B094 99US-013B540 99US-013B19 99US-0139452 99US-0139453 99US-0139454 99US-0139456 99US-0139456 99US-0139459 99US-0139459 99US-0139460 99US-0139461	99US-0132484. 99US-0132486. 99US-0132486. 99US-0132487. 99US-0132487. 99US-0134218. 99US-0134219. 99US-013471. 99US-013476. 99US-013476. 99US-013476. 99US-013523. 99US-013523. 99US-013523. 99US-013523. 99US-013552. 99US-0135782. 99US-0135782.	99US-0121825. 99US-0123180. 99US-0123188. 99US-0125788. 99US-0126785. 99US-0127462. 99US-0128714. 99US-012885. 99US-0128915. 99US-0130077. 99US-0130049. 99US-0130049. 99US-013010. 99US-0131449. 99US-0131449.	(first entry) thaliana protein fragment SEQ ID NO: 63104. tification; signal transduction pathway; metabolic pathway; nassay; genetic mapping; gene expression control; promoter; sequence. thaliana. 2000EP-0301439.
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31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
Drosophila; developmental biology; cell signalling; insecticide;
              Drosophila melanogaster polypeptide SEQ ID NO 14049.
                                            ABB62419;
                                                         ABB62419 standard;
                              26-MAR-2002
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                            (first entry)
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99US-0155596

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                                                        Drosophila sp.
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                                          WO200112126-A2
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DB; ABL06522.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITG-ABLIGOTI), expressed DNA sequences (ABLO1840-ABLIGTS) and the encoded proteins (ABBS7037-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic a genes from Drosophila interactions -
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Hairy protein amino acid sequence.

Cardiac helix-loop-helix factor; CHF; transcription factor; cardiomyocyte; proliferation; myocarditis; myocardial infarction; cardiomyocyte regeneration; anglogenesis inhibitor; differentiation; smooth muscle cell growth; heart disease; hairy.

99US-0148974

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RESULT 13
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                                                                                                                                                                                                                                       Streptomyces sp. CL190; mevalonate pathway; actinomycete; cardiant; isoprenoid compound; osteopathic; cytostatic; ubiquitone; vitamin K carotenoid; heart disease; osteoporosis; cancer; drug; health food.
Seto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHF) polypeptides. CHF is a transcription factor expressed in cardiovascular tissue, which contains a basic helix-loop-helix domain. CHF-1 shares structural homology with hairy, a Drosophila protein essential for the development of the peripheral nervous system. The CHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel cardiovascular helix-loop-helix factor polypeptide and polynucleotide useful for regenerating heart tissue and promoting smooth muscle differentiation to treat heart disease or heart injury -
                              (SETO/) SETO H.
(KUZU/) KUZUYAMA T.
                                                                               08-DEC-1999;
                                                                                                                                               14-JUN-2001
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                                                                                                                                                                                                           Streptomyces sp.
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Takahashi S,
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences encoding them have cardiant, osteopathic and cytostatic activities. The genes are applicable in producing e.g. ubiquitone, vitamin K2 and carotenoids which can be used in the treatment of heart diseases, osteoporosis and cancer in drugs and health foods. The present sequence represents the orfB protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence given in AAH44043 represents a DNA sequence isolated from Streptomyces sp. CL190, containing a base pairs (S1), which encodes the whole enzyme necessary for functioning the mevalonate pathway. The sequence encodes protein sequences, designated orfa to E and hmgr, which are used in the mevalonate pathway. The proteins and polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetes-originated genes of enzymes participating in mevalonate pathway, applicable in producing e.g. ubiquitone, vitamin K2 and carotenoids for treatment of heart diseases, osteoporosis and cancer.
                                                                                                                                                                                                       23-MAR-2000;
11-JUL-2000;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling

invention

and is Disclosure; SEQ ID NO 34890;

21pp + Sequence Listing;

English

genes from Drosophila
interactions -

New isolated nucleic

acid a and

detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell

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RESULT 15
ABB63936
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                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                       insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
Sequence
                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                       New isolated nucleic acid genes from Drosophila and
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                                                                                                                                                                                                         Disclosure; SEQ ID NO 18600; 21pp + Sequence Listing; English
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11-JUL-2000; 2000US-0614150
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Database :
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Copyright (c) 1993 - 2003 Compugen Ltd.
pir1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 2
T52635
T52635
mitogen-activated protein kinase kinase (EC 2.7.1.-) alpha [imported] - Arabidopsis t C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000 C:Accession: T52635

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d Qy	DB 45		Db Ad	CAPAPAPAGE GAPAES	•
30 30	4 4 4	61 61 121 121	Query Match Best Local Matches 34	RESULT 1 A44507 Licheninase (EC 3.2.1.73) - Fibrobact. C:Species: Fibrobacter succinogenes C:Date: 03-Mar-1993 #sequence_revisio: C:Accession: A44507 R:Geather, R.M.; Erfle, J.D. J. Bacteriol. 172, 3837-3841, 1990 A;Title: DNA sequence of a Fibrobacte. A;Reference number: A44507; MUID:9029 A;Accession: A44507 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-349 < TEA> A;Cross-references: EMBL:M33676; NID:0;Keywords: 91ycosidase; hydrolase; p	33000000000000000000000000000000000000
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VNFEH 349 VNFEH 349	DWTEDGNRVDLTDKNI DWTEDGNRVDLTDKNI PASSSVPASSSSAFV	KTSEKHHAVSPAADQA [Length 349; Indels 0; Gaps EVQYGKFEARMKMAAASGTVS	hange 08-Oct-1999 linkage beta-glucanase 6.1; PID:g148576	myb-related transc protein F47F6.1 [i hypothetical prote conserved hypothet hypothetical protein probable methyltra chemotaxis protein probable homeobox probable homeobox protein pro
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A;Reference number: S5963
A;Accession: S59632
A;Molecule type: DNA
A;Residues: 1-621 <MIL>
A;Cross references: EMBL
C;Genetics:
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                                                                                                                                                    endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Cellvibrio mixtus C;Speciles: Cellvibrio mixtus C;Speciles: Cellvibrio mixtus C;Date: 15-Feb-1996 #sequence_revision 11-Apr-1997 #text_change 18-Jun-1999 C;Accession: S59632; S52742
R;Millward-Sadler, S.J.; Davidson, K.; Hazlewood, G.P.; Black, G.W.; Gilbert Blochem. J. 312, 39-48, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AB015316; PIDN:BAA28831.1
C;Gene: ATMKK5
A;Gene: ATMKK5
C;Function:
A;Description: (EC 2.7.1.-); mitogen-activated protein kinase kinase [validated, C;Superfamily; kinase-related transforming protein; protein kinase homology C;Keywords: phosphotransferase; protein kinase
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A:Experimental source: cultivar Columbia; seed
C:Genetics:
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C; Superfamily: kinase-related transforming protein; protein kinase homology
C; Keywords: ATP; phosphotransferase
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A; Accession: T52635
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                    EMBL: 248926; NID: g757808; PIDN: CAA88762.1; PID: g757809
                                                                                                  S59631; MUID:96077124;
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                                                                                                                                                                            K.; Hazlewood, G.P.; Black, G.W.; Gilbert,
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A;Gene: xynB
C:Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linka
A;Pathway: xylan degradation
C;Superfamily: Pseudomonas endo-1,4-beta-xylanase F; Streptomyces e
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence *status predicted <SIG>
F;20-621/Product: endo-1,4-beta-xylanase B *status predicted <MAT>
F;302-615/Domain: Streptomyces endo-1,4-beta-xylanase A homology <S
F;403,516/Active site: Glu *status predicted
                                                                                                                                                                                                                                              A;Title: The Drosophila
A;Reference number: S069
A;Accession: S06956
                                                                                                                                                                                                                                                                                                                                                C;Species: Drosophila melanogaster
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jul-2000
C;Accession: S06956; S06700
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S06956
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A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
B84259
                                      A; Introns: C; Keywords:
                                                                                                                                        C; Genetics
                                                                                                                                                               A;Cross-references: GB:X15904; A;Note: 292-Ser was also found
                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-337 < RUS>
                                                                                                                                                                                                                                                                                                          R; Rushlow, C.A.; Hogan, A.; Pinchin, S.M.; EMBO J. 8, 3095-3103, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Vng1026h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                              A; Map position:
                                                                                                    A;Cross-references: FlyBase:FBgn0001168
                                                                                                                       A;Gene: hairy
                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                       segmentation protein hairy - fruit fly (Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene:
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A; Residues: 1-184 <5
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956; MUID:90059896;
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                                    transcription regulation
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J. Biol. Chem. 268, 13738-13747, 1993
A;Title: Novel use of an iodo-myristyl-CoA analog identifies a semialdehy. A;Reference number: A46600; MUID:93293905; PMID:8514806
A;Status.
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy. A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: A72599
A;Accession: A72599
C;Species: Streptomyces coelicolor C;Date: 22-Oct-1999 #sequence_revision C;Accession: T29064 R;Redenbach, M.; Kieser, H.M.; Denapait
                                                                                                                                                                                                                                                                                                  C; Keywords: coenzyme A; mitoche F; 80-338/Domain: aldehyde dehyd F; 319/Active site: Cys #status
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                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-537 <DEI>
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A; Residues: 1-439 <KAW>
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C;Date: 20-Aug-1999 #sequence_revision
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A;Note: expressed at low levels in a variety of tissues; phosphorylates the peptide s sely related human enzyme, this protein is reported to bind phorbol esters C;Superfamily: protein kinase C mu; protein kinase C zinc-binding repeat homology; pr C;Keywords: Affp; autophosphorylation; duplication; phorbol ester binding; phospholip1 f;1-25/Domain: signal sequence #status predicted <SIG> F;26-918/Product: protein kinase mu #status predicted <AMT> F;145-194/Domain: protein kinase C zinc-binding repeat homology <KZ1> F;277-326/Domain: protein kinase C zinc-binding repeat homology <KZ2> F;587-845/Domain: protein kinase C zinc-binding repeat homology <KZ2> F;587-845/Domain: protein kinase Affp-binding motif F;618,636,712,714/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S42718; S37477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Valverde, A.M.; Sinnett-Smith, J.; Van Lint, J.; Rozengurt, E. Proc. Natl. Acad. Sci. U.S.A. 91, 8572-8576, 1994
A; Title: Molecular cloning and characterization of protein kinase A; Reference number: 148719; MUID:94359973; PMID:8078925
A; Accession: 148719
                                                                                     R;McMorrow, I.; Bastos, R.; Horton, H.; Burke, Biochim. Biophys. Acta 1217, 219-223, 1994 A;Title: Sequence analysis of a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase C (EC 2.7.1.-) mu precursor - mouse N;Alternate names: protein kinase D C:Species: Mus musculus (house mouse) C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996
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A; Molecule type: mRNA
A; Residues: 1-1475 < MCM>
                                          A; Reference number: S42718; MUID: 94154002; A; Accession: S42718
                                                                                                                                                                                                                   nuclear pore complex protein nup153 - human
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A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
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A; Residues: 1-776 < RED>
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A; Residues: 1-918 < RES>
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A;Cross-references: EMBL:Z25535; NID:g406224; PIDN:CAA80982.1;

PID: 9406225

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C:Accession: PN0589

R:Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, Blochem. Biophys. Res. Commun. 195, 158-165, 1993

A;Title: Increased heterogeneity of tyrosine hydroxylase A; Reference number: PN0575; MUID:93371398; PMID:7689834
                tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - gorilla (fragment) % Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hyd: C;Species: Gorilla gorilla (gorilla) C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-2000 C;Accession: PN0590 R;Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
                                                                                                                              RESULT 14
PN0590
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Blochim. Blophys. Acta 495, 388-392, 1977
A;Title: Structure of a peptide antifreeze and mechanism A;Reference number: A03192; MUID:78060969; PMID:588591
A;Accession: A03192
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A; Residues: 1-45 <ICH>
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C;Accession: PN0589
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C:Species: Pseudopleuronectes americanus (winter flounder)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
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 Res.
r.; Fujita, K.; Yoshida, M.;
Commun. 195, 158-165, 1993
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C; Date: 03-May-1994 #sequence_revision 0/-OCT-1994 #Lext_CHAING91
C; Accession: PN0591
R; Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagats Biochem. Biophys. Res. Commun. 195, 158-165, 1993
B; Title: Increased heterogeneity of tyrosine hydroxylase in humans. A; Reference number: PN0575; MUID:93371398; PMID:7689834
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A; Accession: PN0591
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A;Experimental source: lymphocytes of peripheral blood
C;Comment: This enzyme catalyzes the first and rate-limiting step of
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: biopterin; monooxygenase; oxidoreductase
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Hydrolase; SIGNAL

Glycosidase; 1 27

InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; Hydrolase; Glycosidase; Signal; Repeat.

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CHAIN

Query Match
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Mismatches

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Score 349; DB 1; Length 349; Pred. No. 7.9e-311; 16DC4F5BDEFC578A CRC64;

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BETA-GLUCANASE.
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Kirk P.B., Pereira J.P., Bazan F.; "Characterization and structural analysis adaptor protein Wyatt.";
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                                                                    mitted (AFR-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: Adapter involved in the TLR4 signaling pathway in the innate immune response. Acts via IRAK2 and TRAF-6, leading to the activation of NF-kappa-B, MAPKI, MAPK3 and JNK, resulting in cytokine secretion and the inflammatory response (By similarity). SUBUNIT: Homodimer. Also forms heterodimers with MyD88. Binds to TLR4 and IRAK2 via their respective TIR domains. Binds to PKR. Does not interact with IRAK1-1, nor TLR9. SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: CONTAINS 1 TIR DOMAIN.
              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxer B.P., Bhandari D., Bolshakov S.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorlon K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,
ROJER C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAIR_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
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Best Local S
Matches 10
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EMBL; AF410784; AALO5037.1; -.
EMBL; BC005584; AAHO5584.1; -.
MGD; MGI:2152213; Tirap.
Interpro; IPR000157; TIR_domain.
PROSITE; PS50104; TIR; 1.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAIR_DROME STANDARD; PRT; 3
P14003; Q9VSN8;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ish-Horowicz D.;
Ish-Horowicz D.;
"The Drosophila hairy protein acts in both segmentation patterning and shows homology to N-myc.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hairy protein.
H OR CG6494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patterning
EMBO J. 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90059896; PubMed-2479541; Rushlow C.A., Hogan A., Pierchin S.M., Howe K.M., Lardelli M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Oregon-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.9%; ... 1 Similarity 100.0%; 10; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response; Inflammatory response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ASSSSVPASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ing and shows homol 8:3095-3103(1989).
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164
241 AA;
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26035 MW; C387D20229E12265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB; Pred. No. 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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A -> V (I
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0.11;
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                             K.A.,
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A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

M Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Syier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

A Syier S.M., Woodage T., Weinstock G.M., Weissenbach J.,

A Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,

Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.

The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).
                                                                                                                                  DNA_BIND
                                                                                                                                                                                                           PROSITE; PS00038; HLH_1; 1.
PROSITE; PS50888; HLH_2; 1.
Nuclear protein; Developmental protein; Pair-rule
                                                                                                                                                                                                                                                                                             SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
                                                                                                                                                                                                                                                                                                                      EMBL; X15904; CAA34018.1; -. EMBL; X15905; CAA34019.1; -. EMBL; AE003554; AAF50378.1; -.
                                                                                                                                                                                                                                                                                                                                                                            TRANSFAC; T00345; -.
FlyBase; FBgn0001168; h.
InterPro; IPR001992; HLH_basic.
InterPro; IPR003650; Orange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paroush 2., Finley R.L. Jr., Kidd T., Wainwright S.M., Ingha Brent R., Ish-Horowicz D.; "Groucho is required for Drosophila neurogenesis, segmentatisex determination and interacts directly with hairy-related
                                                        DOMAIN
                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95094252; PubMed-8001118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: NUCLEAR.

DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A HELIX-INTERRUPTING FROLINE) THE STO THE N-BOX (CACNAG), RATHER THAN THE CANONICAL E-BOX (CANNTG).

DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: PAIR-RULE PROTEIN THAT REGULATES EMBRYONIC SEGMENTATION AND ADULT BRISTLE PATTERNING. TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH PROTEIN FOR THEIR TRANSCRIPTION (EG. THE FUSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSCRIPTIONAL CO-REPRESSOR RECRUITED HAIRY-RELATED PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WITH A CO-REPRESSOR PROTEIN (GROUCHO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S06956; S06956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79:805-815(1994).
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  32
45
149
222
241
334
292
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  44
89
157
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                                                                                                                                                           regulation; Repressor; BASIC DOMAIN.
POLY-ALA.
WRPW MOTI
S -> P.
                                                                            HELIX-LOOP-HELIX GLN-RICH.
GLN-RICH.
                         MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no rest
                            (REQUIRED
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                                                                                                                                                                                    protein;
Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segmentation,
                            FOR ACTIVITY)
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ri V., Reese M.G.
                                                                                                                                  (BY
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X., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TARGET DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                  SIMILARITY).
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Best Local
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Best Local
                                       Matches
                                                                                                   NP_BIND
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deichaite I., Berthiaume L., Peseckis S.M., Patton W.F., Resh M.D.; "Novel use of an iodo-myristyl-CoA analog identifies a semialdehyde dehydrogenase in bovine liver.";
J. Biol. Chem. 268:13738-13747(1993).
-i- FUNCTION: PLAYS A ROLE IN VALINE AND PYRIMIDINE METABOLISM. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methylmalonate-semialdehyde dehydrogenase [acylating],
precursor (EC 1.2.1.27) (MMSDH).
                                                                                                                                                              PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.

PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; FALSE_NEG.

Oxidoreductase; NAD; Transit peptide; Mitochondrion.

TRANSIT 34 MITOCHONDRION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                       SEQUENCE
                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                               EMBL; L08643; AAA30650.1; PIR; A46600; A46600. HSSP; P51977; 1BXS.
                                                                                                                                                                                                                                                                                                 or send
                                                                                                                                                                                                                                                                                                                                                                                                                                         FATTY ACYL-COA.
-:- CATALYTIC ACTIVITY: 2-methyl-3-oxopropanoate +
propanoyl-coa + CO(2) + NADH.
-:- SUBUNIT: HONODIME3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q07536;
                                                                                                                                                                                                                        Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93293905; PubMed=8514806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALDH6A1 OR MMSDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMSA_BOVIN
                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                    PTM: THE N-TERMINUS IS BLOCKED.
SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Mitochondrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 LAVAAAAA
                                                                                                                                                                                                                      PF00171; aldedh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LAVAAAAAA
                                    Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
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9; Conser
AVAAAAAAL
                                                                                                                                                                                                                                 IPR002086; Aldehyde_dehydr
                                                                                       263
319
126
537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Bovine)
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA;
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319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.6%;
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                                                                                                     BY SIMILARITY ML -> TD (IN )
                                                                                                                                         METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE [ACYLATING].
                                                                                                                           NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; actyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
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                                                                                        69DF39506E62F9C0
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                                       Mismatches
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                                                             Length 537
                                                                                          CRC64;
                                       Indels
                                                                                                      AA SEQUENCE)
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RESULT 5

KPCM_MOUSE
ID KPCM_MOUSE
AC 062101:
DT 16-0CT-2001
DR PRCKM OP PKC
OS MUS MUSCULLU
OC EUMSTVOTE PR
RN [2]
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RN [2]
RT for diacyly
RT for diacyly
RT MOLECULAR
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RT GOMBIN ";
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RT GOMBIN ";
RN [2]
RT GOMBIN ";
RN [2]
RT HOSPHORYLA
RA MACLINE-994
RA PROSITE; PR
RA MACLINE-994
RA MACLINE-994
RA MACLINE-994
RA MACLINE-994
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RA MACLINE-994
RA PROSITE; PR
RA MACLINE-994
RA MACLINE-9
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16-OCT-2001 (Rel. 40, Last s
15-JUN-2002 (Rel. 41, Last a
Protein kinase C, mu type (E
PRKCM OR PKD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002219; DAG_
Interpro; IPR000719; Euk_
Interpro; IPR001849; PH.
Interpro; IPR002290; Ser_
Pfam; PF00069; pkinase; 1
                          SMART; SM00109; C1; 2.

SMART; SM00220; PH; 1.

SMART; SM00220; S_TKC; 1.

PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.

PROSITE: PS50081; DAG_PE_BIND_DOM_2; 2.

PROSITE: PS50003; PH_DOMAIN; 1.

PROSITE: PS500107; PROFEIN_KINASE_ATP; 1.

PROSITE: PS00108; PROFEIN_KINASE_ST; 1.

PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

ATP-binding; Transferase; Serine/threonine-protein kinase;

ATP-binding; Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/c: TISSUE-Lung;
MEDLINE-94359973; PubMed-8078925;
Valverde A.M., Sinnet-Smith J., Van Lint J., Rozengurt E.;
"Molecular cloning and characterization of protein kinase D: a target of diacylglycerol and phorbol esters with a distinctive catalytic domain ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00008; DAGPEDOMAIN. ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00130; DAG
Pfam; PF00169; PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 234524; CAA84283.1;
HSSP; P28867; 1PTQ.
MGD; MGI:99879; Prkcm.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matthews S.A., Rozengurt E., Cantrell D.;
"Characterization of serine 916 as an in vivo autophosphorylation site for protein kinase D/Protein kinase Cmu.";
J. Biol. Chem. 274:26543-26549(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99403106; PubMed=10473617;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10090;
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FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,

SERINE- AND THREONINE-SPECIFIC ENZYME.

ENZYME REGULATION: ACTIVATED BY DIACYLGLYCEROL AND PHORBOL ESTERS.

PTM: Autophosphorylated.

SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING DOMAINS.
SIMILARITY: CONTAINS 1 PH DOMAIN.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long as its content is in no way id and this statement is not removed. Usage by and for commercial is requires a license agreement (See http://www.isb-sib.ch/announce/lan email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAG_PE-bind;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40, Last sequence update)
41, Last annotation update)
mu type (EC 2.7.1.-) (nPKC-mu) (Protein kinase D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAG_PE-bind.
Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ser_thr_pkinase.
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   Repeat;
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   Phosphorylation
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01-OCT-1996
15-JUN-2002
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BINDING
ACT_SITE
MOD_RES
                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                    N153_HUMAN
P49790;
                                      Pfam; PF00641; zf-RanBP; 4.
SMART; SM00547; ZnF_RBZ; 4.
PROSITE; PS01358; ZF_RANBP2_1; 4.
PROSITE; PS50199; ZF_RANBP2_2; 4.
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                     Genew; HGNC:8062; NUP153
                                                                                                                                                                               This SWISS-PROF entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics firstitute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nuclear pore complex protein Nupl53 (Nucleoporin Nupl53) (153 kDa
                                                                                                               EMBL; Z25535; CAA80982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleoporin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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 ZN_FING
          DOMAIN
                      DOMAIN
                               Nuclear
                                                                                           MIM; 603948;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                NUP1, NSP1, POM 121 AND MAMMALIAN P62.
SIMILARITY: CONTAINS 4 RANBP2-TYPE ZINC FINGERS.
                                                                                                                                                                                                                            DOMAIN: CONTAINS F-X-F-G REPEATS.
SIMILARITY: THE REPEAT REGION COMPOSED OF PENTAPEPTIDE REPEATS SEPARATED BY SER/THR-RICH DOMAINS IS SIMILAR TO THAT OF YEAST NUP1, NSP1, POM 121 AND MAMMALIAN P62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVAAAAAL
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                                                                               IPR001876; Znf_RanGDP
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916
918
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277
428
589
198
595
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1 547
1 547
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201
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Transport;
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687
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         ; Repeat; Zir
GLY-RICH.
POLY-GLY.
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   RANBP2-TYPE
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                               Zinc-finger;
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                               DNA-binding
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ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                  P04002;
23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleoste Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectidei; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Antifreeze peptide 3.
Pseudopleuronectes americanus (Winter
                       SEQUENCE FROM N.A. MEDLINE-82197490;
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
                                                                                                                                                                                                                                                       Antifreeze protein A/B precursor. Pseudopleuronectes americanus (Wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANP3_PSEAM
P02733;
     Davies
                                                                                                                                                                                                                                  americanus).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=78060969;
Devries A.L., Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      americanus)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chim. Biophys. Acta 495:388-392(1977).
FUNCTION: ANTIFREEZE PROTEINS LOWER THE BLOOD
SIMILARITY: BELONGS TO THE TYPE-I APP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL A03192; FDFL3W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
     P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
8; Conserv
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Similarity 100.0%;
9; Conservative
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37 AA; 3144 MW; 46AA951A962DECA9
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     Roach
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  PubMed=6952188;
h A.H., Hew C.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
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Y.;
                                                     (PROTEIN
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RANBP2-TYPE 3.
RANBP2-TYPE 4.
MW; 3CB415A6909DF80E C
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Pred. No. 4.3
0; Mismatches
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Pred. No
                                                                                                                                                                                                                                                          (Winter flounder) (Pleuronectes
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Sicheri F., Yang D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davies
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PIR; A03194; FDFLAW.
PIR; A05161. A05161.
PIR; S02326; S02326.
PIR; JS0704; JS0704.
PDB; 1ATF; 15-OCT-94.
PDB; 1WFB; 03-JUN-95.
PDB; 1WFB; 03-JUN-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               winter flounder.";
Nature 375:427-431(1995).
Nature 375:427-431(1995).
-I- FUNCTION: ANTIFFEEZE PROTEINS LOWER THE BLOOD FREEZING PO-
-I- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF PROTEIN A.
-I- SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY. TYPE 1 AFP
ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.
                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88259236; PubMed-3133486;
Scott G.K.; Davies P.L., Kao M.H., Fletcher G.L.;
"Differential amplification of antifreeze protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Ice-binding structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-RAY CRYSTALLOGRAPHY (1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Conservation of antifreeze
                                                                                                                                                                                                                                                                                    L00138; AAB55964.1;
L29178; AAB55964.1;
M62414; AAA49469.1;
L207506; CAA30389.1;
M62416; AAA49471.1;
M62417; AAA49472.1;
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                                                                                                                                   pr00308; ANTIFREEZEI.
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64559; PubMed=6086629;
, Hough C., Scott G.K., Ng N., White B
protein genes of the winter flounder.
em. 259:9241-9247(1984).
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                                                                                                                  family; Signal; 3D-structure
PROTEIN REF. 2).
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Best Local S
Matches 8
 Q9CCP3;
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16-OCT-2001
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SEQUENCE
                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symblotic bac Mesorhizobium loti.";
                                                                                                                                                                                                      Ribosomal protein; Complete proteome SEQUENCE 133 AA; 14358 MW; 63D98
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision;
Phyllobacteriaceae; Mesorhizobium.
                                                         RISB_MYCLE
                                                                                                                                                                                                                          TIGREAMS; TIGR00002; S16; 1.
PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG
                                                                                                                                                                                                                                                              Pfam; PF00886; Ribosomal_S16;
                                                                                                                                                                                                                                                                      EMBL; AP003004; BAB51050.1; -.
InterPro; IPR000307; Ribosomal_S16.
                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-MAFF303099;
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Q98E70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
30s ribosomal protein $16.
Res. 7:331-338(2000).
SIMILARITY: BELONGS TO THE S16P
                                                                                                                 116
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Similarity 100.0%
8; Conservative
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s; TIGR00002; S16; 1
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Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                               FAMILY OF RIBOSOMAL PROTEINS.
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o. 4.5;
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Drosophila
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B 3 5 5 5 5

sechellia (Fruit fly),

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Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.
Holroyd S., Hornsby T., Jagels K., Lacroix C., MacLean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simmon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
"Maccion."
                                                                    15-JUL-1998
15-JUL-1998
30-MAY-2000
                                                                                                                                         ZEST_DROMA S
Q24597; Q24598;
Q27387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             radssive gene decay in the leprosy bacillus.", Nature 409:1007-1011(2001).
                                            Regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riboflavin biosynthesis; Transferase; Complete proteome DOMAIN 140 146 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD003664; DMRL_synthase; 1.
TIGRFAMs; TIGR00114; ribH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Lumazine synthase) (Riboflavin synthase beta chain). RIBH OR ML0560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leproma; ML0560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'.D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'.D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).

CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine riboflavin 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.

PATHWAY: Riboflavin biosynthesis; last step.

SIMILARITY: BELONGS TO THE DWRL SYMTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conser
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mauritiana
                                               protein
                                   (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 39, Last annotation updat
protein zeste (Fragment).
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                                                                                                                                                              STANDARD; ; Q24599; (
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RESULT 12
ALL4_ASPFU
ID ALL4_ASPFU
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Best Local S
Matches
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Population genetics and phylogenetics of DNA sequence variation at multiple loci within the Drosophila melanogaster species complex.";
MOI. Biol. Evol. 10:804-822(1993).
-i- FUNCTION: INVOLVED IN TRANSVECTION PHENOMENA (= SYNAPSIS-DEPENDENT GENE EXPRESSION), WHERE THE SYNAPTIC PAIRTING OF CHROMOSOMES CARRYING GENES.WITH WHICH ZESTE INVERACTS INFLUENCES THE EXPRESSION OF THESE GENES. ZESTE BINDS TO DNA AND STIMULATES
                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                                                              DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93360802;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSCRIPTION FROM A NEARBY PROMOTER (BY SIMILARITY).
SUBUNIT: SELF-ASSOCIATE FORMING COMPLEXS OF SEVERAL HUNDRED MONOMERS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear (By similarity).
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L13057;
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L13055;
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8; Conser
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FBgn0012801; Dsec\z.
FBgn0012904; Dsim\z.
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268
268
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AAA29033 1

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97
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268
30353
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                                                                                                                                                                                                                                                    regulation;
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                                                                                                                                                                                                    SPECIFIC, WITH ZESTE LOCUS.
GLN/ALA-RICH (OPA-REPEAT INVOLVED IN
TRANSCRIPTIONAL ACTIVATION OR REPRESSION
   PRT;
                                                                                                                                                       F592F8FA4F2DB47B CRC64;
                                                                                                                                                                              DIFFERENT TARGET LOCI)
SSING (IN STRAIN SI-K2).
                                                                                                          Mismatches
                                                                                                                     No.
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CYSD_RHIME
ID CYSD_RHIME
AC P56892;
DT 30-MAY-2000
DT 30-MAY-2000
DT 15-JUN-2002
DE Sulfate ader
CO SULFATE ACC
OS Rhizobium me
OC Rhizobium me
OC Rhizobium me
OC Rhizobium me
OC RHIZOBIUM P1
OC RHIZOBIUM ME
OC STRALN=1021,
RX MEDLINE=993
RA Abola A.P.,
RT "Reduction oc
RT RHIZOBIUM ME
RI J. Bacterial
RN SEQUENCE FR
RC STRALN=1021,
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RN GODGIN D.,
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RA BOLSTART T.,
RA REDAT T.,
RA REDAT C.,
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Best Local
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30-MAY-2000 (Rel. 39, Createu,
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allergen.
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Allergen Asp f 4 (Fragment).
Aspergillus fumigatus (Sartorya fumigata).
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomy
Burotiales; Trichocomaceae; mitosporic Trichocomaceae;
                  MEDLINE=21396507; FubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batul Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux Boistard P., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium meliloti (Sinorhizobium meliloti). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hemmann S., Nikolaizik W.H., Schoeni M.H., Blaser K., Crameri R., "Diagnosis of allergic bronchopulmonary aspergillosis in patients cystic fibrosis by IgB-specific serology with recombinant Aspergifumigatus allergens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 42202 / AF-102;
                                                                                                                                                                                                                  Abola A.P., Willits M.G., Wang R.C., Long S.R.; "Reduction of adencsine-5'-phosphosulfate instead of 3'-phosphosubrate in cysteine biosynthesis by phosphoadencsine-5'-phosphosulfate in cysteine biosynthesis by Rhizobium meliloti and other members of the family Rhizobiaceae.";
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                          STRAIN=1021
                                                                                                                                                                                                                                                                                               MEDLINE=99395034; PubMed=10464198;
                                                                                                                                                                                                                                                                                                                       STRAIN-1021;
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                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=382;
  Analysis of the
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                                                                                                                                                                                                    Bacteriol.
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8; Conserv
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                                                                                                                                                                                                181:5280-5287(1999).
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  chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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  sequence of
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  the Legume
                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobiaceae group
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Best Local
                                                                                                                                                                                                                       Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Bart. E., III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YE80_MYCTU STANDARD; PRT; 317 AA P71761; O53171; O1-NOV-1997 (Rel. 35, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical protein Rv1480. RV1480 OR MT1527 OR MTV007.27 OR MTCY277.01 MYCODARCTERING TUBERCULOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                          SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eiser
Fleischmann R.D., Alland D., Eiser
Peterson J., DeBoy R., Dodson R.,
Kolonay J.F., Nelson W.C., Umayam
Delchar A., Utterback T., Weldman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cysteine biosynthesis; Transferase; Nucleotidyltransferase; Complete proteome. CONFLICT 260 260 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98.9877-9882(2001).

-!- CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylylsulfate.
-!- PATHWAY: FIRST STEP IN THE SULFATE ACTIVATION PATHWAY. THIS
REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
BIOSYNTHETIC PATHWAY.
-!- SUBUNIT: HETERODIMER COMPOSED OF CYSD, THE SMALLER SUBUNIT, AND
CYSN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria;
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                       lshai W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243
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PF01507; PAPS_reduct; 1.
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genome comparison
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8; Conserv
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317 AA;
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of Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinobacteria (class); Actinobacteridae;
                                       ., Eisen J.A., Carpenter L., White O., son R., Gwinn M.L., Haft D., Hickey E., Umayam L.A., Ermolaeva M.D., Salzberg Weldman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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Pred. No.
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093F2724D22841CB
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ВВ
tuberculosis
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clinical and
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Matches 8
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087125;
30-MAY-2000
16-OCT-2001
15-JUN-2002
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EMBL; AE007022; AAK45
TIGR; MT1527; -
TubercuList; Rv1480;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Protein-glutamate methylesterase (EC 3
CHEB OR PA1459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-99161288; PubMed-10052136;
Kato J., Nakamura T., Kuroda A., Ohtake H.;
"Cloning and characterization of chemotaxis genes
"Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and aeruginosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biosci. Biotechnol.
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Hypothetical protein; Complete
SEQUENCE 317 AA; 34333 MW;
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InterPro; IPR002035; V
Pfam; PF01882; DUF58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laboratory strains.";
Submitted (APR-2001)
                                                                                                                                           FUNCTION: INVOLVED IN THE MODULATION OF THE CHEMOTAXIS SYSTEM; CATALYZES THE DEMETHYLATION OF SPECIFIC METHYLGLUTAMATE RESIDUES INTRODUCED INTO THE CHEMORECEPTORS (METHYL-ACCEPTING CHEMOTAXIS
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Matches 8; Conserv
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EMBL; AE004575; AAG04848.1; -.
HSSP; P04042; ICHD;
InterPro; IPR000673; CheB_methylest.
InterPro; IPR001799; Response_reg.
Pfam; PF00072; response_reg; 1.
Pfam; PF01339; CheB_methylest; 1.
ProDom; PD005039; Response_reg; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- DOMAIN: THE N-TERMINAL REGULATORY DOMAIN INHIBITS THE ACTIVITY OF THE C-TERMINAL EFFECTOR DOMAIN.
-!- PTM: PHOSPHORYLATED BY CHEA. PHOSPHORYLATION SUPPRESSES THE INHIBITORY ACTIVITY OF THE N-TERMINAL DOMAIN (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
-!- SIMILARITY: CONTAINS 1 CHEB-TYPE METHYLESTERASE DOMAIN.
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PROSITE; PS50110; RESPONSE_REGULATORY; 1.

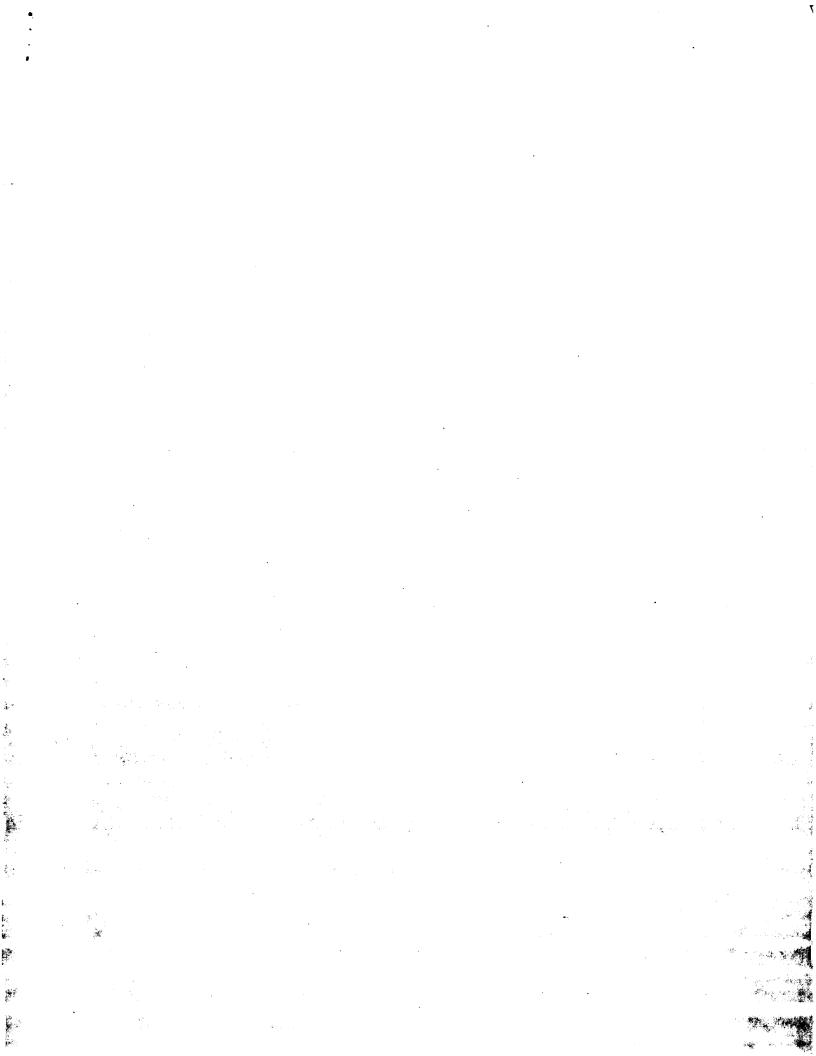
Hydrolase; Chemotaxis; Sensory transduction; Phosphorylation;
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CHEB-TYPE METHYLESTERASE.

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Q9SR71;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
T2ZK18.10 protein (Putative TBP-associated 58 kDa subunit
                                                  Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC010927; AAF04417.1; .
EMBL; AF344878; AAR28289.1; .
InterPro; IFR004822; Histone_core.
InterPro; IFR002965; P_rich_extensn.
InterPro; IFR003228; TFIID_sub.
PRINTS; PR01217; PRICHEXTENSN.
PRODOM; PD012998; TFIID_sub; 1.
SEQUENCE 539 AA; 57710 MW; 72597A2E1B57EE9B CRC64;
                                                                                                                                                                                                                                                                             Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Hass Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnst Bowman C.L., White O., Nierman W.C., Fraser C.M., "Arabidopsis thaliana chromosome III BAC T22K18 genomic submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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T22K18.10 OR TAFII58.
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InterPro; IPR003243; Cystatin_C/M.
Pfam; PF00031; Cystatin; 2.
ProDom; PD001231; Cystatin; 2.
ProDom; PD001231; Cystatin_C/M; 1.
SMARP; SM00043; CY; 1.
SMARP; SM00043; CY; 1.
PROSITE; PS00287; CYSTATIN; UNKNOWN_1.
SEQUENCE 250 AA; 27269 MW; 6F2A7D4E8BBAF66F CRC64;
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Q9LJ08;
01-OCT-2000 (
                                                            SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M., Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Chenk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Karkim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki Ngakurai T., Theologis A., Davis R.W.;

ECker J., Theologis A., Davis R.W.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
clone:p0667A10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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01-JUN-2002 (TrEMBLrel.
ESTS AU67919(C10906).
       SEQUENCE
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   Ą.
   37048
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(GA3) genomic
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   0D65B7F67D698521 CRC64;
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080398;
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01-MAR-2002
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EMBL; Y07694; CAA68958.1; -. HSSP, P24941; IBUH.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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PROSITE; PS50011; PROTEIN_KINASE_DOM;
ATP-binding; Kinase; Transferase.
SEQUENCE 348 AA; 38329 MW; C18C98;
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ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
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InterPro; IPR002290;
Pfam; PF00069; pkinas
                                                           MAP kinase
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"Molecular characterization and expression
L. WAP kinase kinase cuna AtMAP2Kalpha.";
Plant Sci. 140:41-52(1999).
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                  Arabidopsis
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Molecular cloning
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kinase alpha protein kinase (EC 2.7.1.
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(Mouse-ear cress).
ntae; Streptophyta;
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Eukaryota;

Embryophyta; Tracheophyta;

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004322;
01-JUL-1997
01-JUL-1997
01-MAR-2002
MYB-related
T02004.16.
                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyla;edons; core eudicots; Rosidae;

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                      STRAIN=CV. COLUMBIA; Rounsley S.D., Lin X Fuhrmann J.L., White Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. /: 131
                         STRAIN=COLUMBIA;
                                              SEQUENCE FROM
                                                                                    Submitted (JUL-1997)
                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                            NCBI_TaxID=3702;
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SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein ki
SEQUENCE 348 AA; 38329 MW; 216C96728F34B5B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P24941; 1AQ1.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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MEDLINE=20277480;
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"Molecular cloning and characterization of cDNAs encoding mitogen-
activated protein kinase kinase in Arabidopsis thaliana.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura
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eurosids II; Brassicales; Brassicaceae; Arabidopsis
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AB023045;
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LARITY: BELONGS TO '015316; BAA28831.1;
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transcription activator (MYBST1) ISOLOG
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Kerlavage A.R., Adams
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EMBL/GenBank/DDBJ
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RESULT OF SOLUTION                                                                                                                            EMBL: 24892b; ....

EMBL: 24892b; ....

HSSP; P14768; ICLX.

InterPro; IPR005088; CBM_15.

R InterPro; IPR001000; Glyco_hydro_10.

P Ffam; PF03426; CBM_15; 1.

DR Pfam; PF0331; Glyco_hydro_10; 1.

DR PRINTS; PR00134; GLHYDRIASE10.

DR PROSTTE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.

DR PROSTTE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.

DR PROSTTE; PS00591; Glyco_hydro_188; Signal; Xylan degradation.

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InterPro; IPR001805; Znf_CCHC.
Pfam; PF00249; myb_DNA-binding; 1.
SMART; SM00395; SANT; 1.
SMART; SM00343; Znf_C2HC; 1.
SMART; SM00343; Znf_C2HC; 1.
PROSITE; PS50090; MYB_3; 1.
DNA-binding; Nuclear protein.
SEQUENCE 369 AA; 40043 MW; DCC03950
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gilbert H.J., Clarke J.H.;
"Novel cellulose-binding domains, NodB homologues and conserved modular architecture in xylanases from the aerobic soil bacteria pseudomonas fluorescens subsp. cellulosa and Cellvibrio mixtus.";
Biochem. J. 312:39-48 (1995).
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MIXTUS;
MEDLINE=96077124; PubMed=7492333;
Millward-Sadler S.J., Davidson K.,
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-i- SIMILARITY: CONTAINS 1 |
EMBL; AC001645; AAE63650.1;
EMBL; AB023046; BAE01274.1;
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Pred. No.
                                                                                                                 Score 10;
Pred. No.
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                                                                                                                                          Length 621;
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    Best Local Similarity
Matches 9; Conserv
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"Oryza satīva nipponbare(GA3) genomic DN
clone:OSZNBA0086P08.";
Submitted (AUG-2000) to the EMBL/GenBank
EMBL; AP001539; BAA92926.1;
EMBL; AP002855; BABA17144.1;
EMBL; AP002855; BABA17144.1;
SEQUENCE 87 AA; 9123 MW; F3ACD82BA63
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. NIPPONBARE;
STRAIN-CV. NIPPONBARE;
Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hil
Brenner M., Burgess S., Hance M., Shvartsbeyn M.
Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.
Utterback T.R., Feldblyum T.V., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:p0708G02.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LI13;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 15, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence
                                                                                                                                                                     Hypothetical protein. SEQUENCE 105 AA; 1
                                                                                                                                                                                                                                               "Oryza sativa chromosome 3 BAC OSJNBb0093E13 Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; ACC91123; AAK72898.1; -
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
Hypothetical 10.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                  White O., Fraser C.M.;
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STRAIN-CV. NIPPONE
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        Conservative
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                                                                                                                                                                              10143 MW;
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                                           Score 9;
Pred. No
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        Mismatches
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i G., Vanaken
J., Salzberg S
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DT V1910
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RP SEQUE
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RA Isena
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Best Local S
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                                                                                   "Cloning of a gene cluster encoding enzymes respons mevalonate pathway from a terpenoid antibiotic-proc strain.";

submitted (FEB-2000) to the EMBL/GenBank/DDBJ datal EMBL; AB037907; BAB07818.1:
InterPro; IPR001745; GHMPknse_ATP.
Pfam; PF00288; GHMP_kinases; I.
TIGRFAMS; TIGR01240; mevDPdecarb; 1.
SEQUENCE 300 AA; 30865 MW; 17D9F9D707781997 CR
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Q9KWF8;
Q1-OCT-2000
01-OCT-2000
01-JUN-2002
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01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=20504483; PubMed=11016950;
Mg W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                   Dairi T.;
"Cloning o
                                                                                                                                                                                                                                                                                                                                                                                       Kitasatospora griseola (Streptomyces griseolosporeus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Kitasatospora
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VNG1026H.
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NCBI_TaxID=64091;
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O (TrEMBLrel. 21, Last annotation
diphosphate decaroboxylase.
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ilarity 100.0%;
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aeota; Halobacteria;
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Best Local 9
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                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999
01-NOV-1999
01-JUN-2002
                        SEQUENCE FROM N.A. STRAIN-R3-24, R3-2, R3 Robin C., Lyman R.F.,
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Interpro; IPR003597; Ig.cl.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR001000
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MEDLINE=20093998; PubMed=10630302;
Seo J.W., Bontrop R., Walter L., Guenther E.,
"Major histocompatibility complex-linked MIC genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; V.
Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Papio.
NCBI_TaxID=9557;
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01-DEC-2001
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    Polymorphism at hairy associated
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SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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PF00129; MHC_I; 1.
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PD000050; MHC_I; 1.
SM00407; IGc1; 1.
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A.D., Langley
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Last sequence update)
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Pred. No
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  Langley
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8, R3-95, AND R3-74; ey C.H., Mackay T.F.C variation in Drosoph:
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Best Local
Matches
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Best Local
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Submitted (SEP-2001) to the EMBL MND55842; AAL17776.1; -...
EMBL; AY055836; AAL17771.1; -...
EMBL; AY055837; AAL17771.1; -...
EMBL; AY055838; AAL17773.1; -...
EMBL; AY055838; AAL17773.1; -...
EMBL; AY055841; AAL17774.1; -...
EMBL; AY055841; AAL17775.1; -...
EMBL; AY055841; AAL17775.1; -...
                                                       Q9KWG4
Q9KWG4;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2002
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Q95NH3;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2002
Diphosphomevalonate decarboxylase. Streptomyces sp. (strain CL190). Bacteria; Firmicutes; Actinobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophillidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hairy.
H OR CG6494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bristle number.";
Submitted (SEP-2001) to the
EMBL; AY055835; AAL17769.1;
EMBL; AY055833; AAL17767.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=R3-6, R3-105, AND R3-107;
Robin C., Lyman R.F., Long A.D., L
"Polymorphism at hairy associated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0001168; h.
InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1
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; 37021 MW; E08B90F942B245C0
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Search completed: July 11, 2003, 11:06:08 Job time: 82 secs
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SEQUENCE FROM N.A.

CONTRAIN-CL190;

XX MEDLINE-20353446; PubMed-10894721;

XX Takag1 M., Kuzuyama T., Takahashi S., Seto H.;

YA gene cluster for the mevalonate pathway from Streptomyces sp.

XY Strain CL190."; Carrier for the mevalonate pathway from Streptomyces sp.

XY Bacteriol. 182:4153-4157(2000).

XI J. Bacteriol. 182:4153-4157(2000).

XI J. Bacteriol. 182:4153-4157(2000).

XI J. Bacteriol. 182:4153-4157(2000).

XI Interpro; IPR001745; GHMPkns-ATP.

XI Interpro; IPR001745; Mev_gal_kin.

XI Interpro; IPR001745; Mev_gal_kin.

XI Pfam; PF00288; GHMP kinases; 1.

XI Pfam; PF00288; GHMP kinases; 1.

XI Pfam; PF00289; MEVGALKINASE

XI TIGRFAMS; TIGR01240; mevDPdecarb; 1.

XI SEQUENCE 350 AA; 36409 MW; 1CE61F306ACDC7CF CRC64;
                                                                                                                                                                                                                                                         Query Match 2.6%; Score 9; DB 2; Best Local Similarity 100.0%; Pred. No. 4.6; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=93372;
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130 ALAVAAAAA 138
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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US-08-975-166-8
US-08-975-166-9
US-08-975-166-9
US-09-117-121-42
US-09-117-121-42
US-09-1184-220-1
US-07-814-220-1
US-07-814-220-1
US-07-814-220-1
US-07-814-2331-13
US-07-814-231-13
US-09-100-664A-3
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                                 Sequence 12, Appli Sequence 1, Appli Sequence 1, Appli Sequence 9, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 1, Appli Sequence 4, Appli Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli Sequence 5, Appli Sequence 6,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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US-09-286-690-12
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Best Local Sim
Matches 228;
Sequence 152, Application US/08159339A Patent No. 6037135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 12
LENGTH: 228
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Result

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Minimum Maximum

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ALIGNMENTS	US-09-170-996-22	US-08-609-049A-22	US-08-853-659A-39	US-09-325-932A-144	US-09-344-529-2	US-08-317-844B-52	US-08-425-069-52	5422425-9	US-09-528-706-103	US-09-586-472-103	US-08-516-859A-103	.5422425-10	US-08-721-458B-42	US-08-503-226B-42	US-08-061-376-5	PCT-US96-02331-15	US-08-195-152-2	US-08-864-038A-3
	Sequence 22, Appl	Sequence 22, Appl .	Sequence 39, Appl	Sequence 144, App	Sequence 2, Appli	Sequence 52, Appl	Sequence 52, Appl	Patent No. 5422425	Sequence 103, App	Sequence 103, App	Sequence 103, App	Patent No. 5422425	Sequence 42, Appl	Sequence 42, Appl	Sequence 5, Appli	Sequence 15, Appl	Sequence 2, Appli	Sequence 3, Appli

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; TYPE: PRT
; ORGANISM: Fibrobacter succinogenes
US-09-286-690-12
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CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
181 PLEQFINWYKYTPGQGEGGSDETLDWTDNEDTEDGSRWGKGDWTF 228
                                                                            121 FHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKL
                                                                                                       121 FHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKL
                                                                                                                                                                                                                                                                                  SMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQA
                                                                                                                                                                                SMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQA
                                                                                                                                                                                                                                                                                                                                                                                          65.3%; Score 228; DB 3; L ilarity 100.0%; Pred. No. 4.8e-215; Conservative 0; Mismatches 0;
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Gaps

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180

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Query Match
Best Local Similarity
Thiches 8; Conserve
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                                                                                                                                                                                                                                                           US-08-180-524-1
                                                                                                                                                                                                    Sequence 1, Application US/08180524 Patent No. 5849537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cells, ESCENT.
TITLE OF INVENTION: HLA BI
TITLE OF INVENTION: Uses
TITLE OF SECUENCES: 1254
        APPLICANT: Kot, Edward
APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WEDER, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FBSTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
NUMBER OF
                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0
FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                          13 AVAAAAAA 20
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Sette, Alessandro
Celis, Esteban
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linear
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100.0%; Pr
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0; Mismatches
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; ORIGINAL SOURCE:
; ORGANISM: Pseu
US-08-180-524-1
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                                                                                                                                                                                                                                                                                                             RESULT 4
                                                                                                                                                                                                                                                           Sequence 8, Application US/08180524 Patent No. 5849537
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                            APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF E
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (414) 277-5591 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPULCE: P
MOLECULE TYPE: P
HYPOTHETICAL: NO
                                                                                                                                             APPLICANT:
               CORRESPONDENCE ADDRESS:
ADDRESSEE: Thad Kryshak, Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: MSWORD Version 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 28-FEB-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                            APPLICANT:
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                                              NUMBER OF SEQUENCES:
                                                                                                                                                                             APPLICANT:
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CITY: Milwaukee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: APPLICATION NUMBER:
   STREET:
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411 East Wisconsin Avenue
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Lusk, Lance
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0; Mismatches
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                                                                              EXPRESING ANTIFREEZE PROTEINS
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STATE: COUNTRY:

Wisconsin

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Query Match
Best Local Similarity
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US-08-180-524-9
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9,
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APPLICATION NUMBER: US 07/409,233

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217

FILING DATE: 19-SEP-1989

ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66-005-923/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (414) 277-5707
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                              APPLICANT: Kot, Edward
APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
ANTI-SENSE: 1
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     APPLICANT:
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                  COUNTRY: USA
ZIP: 53202
                                                  CITY: Milwaukee
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/917,216 FILING DATE:
                                                                                   STREET:
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STRANDEDNESS: sir
                                                                                                    ADDRESSEE:
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                                                                               411 East Wisconsin Avenue
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Lusk, Lance
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linear
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Huige, Nick
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                                                                                                      Thad Kryshak, Quarles & Brady
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US-08-975-166-1
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GENERAL INFORMATION:
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY,AGENT INFORMATION:
NAME: KTYSHAK, Thad
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66-005-9234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5591
INFORMATION FOR SEQ ID NO: 9:
COURAGING OF TELEPACE (414) 277-5591
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                         ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                STREET: 41.
STREET: MILWALKEE
CTATE: Wisconsin
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Thad Kryshak, Quarles & Brady
STREET: 411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
SOFTWARE: MSWORD CURRENT APPLICATION
                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
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                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                     Chicoye, Etzer
Barney, Michael C.
Bower, Patricia A.
Cronan, Charles L.
Cronan, Charles L.
WENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
AVENTION: IN YEAST
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Huige, Nick
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                   Version 5.0
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0; Gaps

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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

US/08/180,524

CLASSIFICATION: 435

FILING DATE:

APPLICATION NUMBER: US/08/975,166 FILING DATE:

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; ORGANISM: Pseudopleuronectus americanus
US-08-975-166-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-975-166-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08975166 Patent No. 5928877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   APPLICANT: KOT, Edward
APPLICANT: Chicoye, Etzer
APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thad Kryshak, Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                  STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/917,216 FILING DATE:
 APPLICATION NUMBER:
                                                                                                                                     COUNTRY:
                                                                                                                                                                           CITY: Milwaukee
                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35,433
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                                                                                                                       53202
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Similarity 100.0%;
8; Conservative
                                                                                                                                                                                        411 East Wisconsin Avenue
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Lusk, Lance
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US/08/975,166
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o. 1.1;
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US-08-975-166-9
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Best Local Similarity
Matches 8; Conserv
                                                  ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: pro
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LENGTH: 37 amino acids
TYPE: amino acid
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APPLICATION NUMBER:
FILING DATE: 19-SEP-
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
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             APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                 STREET: 411 East
CITY: Milwaukee
STATE: Wisconsin
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                                                                                                                                                       COUNTRY: USA
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5. 5928877
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Chicoye, Etzer
Barney, Michael C.
Bower, Patricia A.
Cronan, Charles L.
Cronan, Charles L.
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19-SEP-1989
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100.0%; Pred. No. 1.1;
htive 0; Mismatches
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                                         US/08/975,166
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APPLICATION NUMBER: FILING DATE:

US/08/180,524

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Best Local Similarity
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US-09-117-121-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                          APPLICATION NUMBER: WO PCT/CA97/00062
FILING DATE: 30-JAN-1997
ATTORNEY/ACENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 016252-001610U:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (414) 277-559
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
TELEFAX: (4
                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,121
FILING DATE: 20-NOV-1998
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hew, Choy
APPLICANT: Gong, Zhiyuan
TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
TITLE OF INVENTION: and Nucleic Acids
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
TELEFAX: (414) 277-5591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,433
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No. 6307020
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                (415)
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-- NO: 9:
              576-0300
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%; Pred. No. 1.1
0; Mismatches
                                                                  016252-001610US
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5. 1.1;
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                Query Match
Best Local Similarity
""" 8; Conserv
                                                                                    ; MOLECULE TYPE: protein US-09-117-121-42
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US-09-117-121-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6307020 GENERAL INFORMATION:
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                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NERAL INFUNENCE: Choy APPLICANT: Hew, Choy APPLICANT: Gong, Zhiyuan TITLE OF INVENTION: Intracellular AntiTITLE OF INVENTION: and Nucleic Acids
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 37 aminc acids
                                                                                                                                                                                                                                                                                        FILING DATE: 20-NOV-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CA97/00062
FILING DATE: 30-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..37
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                           LENGTH:
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AAAAAALT 22
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Conservative (
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100.0%; Pr
100.0%; O;
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                                        Score 8;
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                              Mismatches
                                           NO.
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                                          DB 4;
o. 1.1;
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                              Indels
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; OTHER INFORMATION: (wflarP-6)
US-09-344-529-4
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US-07-814-220-1
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Best Local Similarity 100.
                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION #1.30
CURSCRECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
APPLICATION STATEMENT WINDSCALES
APPLICATION HUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/07814220 Patent No. 5925540 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 4
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APPLICANT: HSC Research and Development Limited Partnership
TITLE OF INVENTION: Sculpin-Type Antifreeze Polypeptides and Nucleic Acids
FILE REFERENCE: 016352-002620US
CURRENT APPLICATION NUMBER: US/09/344,529
CURRENT FILING DATE: 1999-06-24
COURRENT FILING DATE: 1999-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: US 60/090,794
EARLIER FILING DATE: 1998-06-26
EARLIER APPLICATION NUMBER: US 60/095,713
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Caceci, Thomas
APPLICANT: Toth, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Reston
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: WHITHAM, CURTIS & WHITHAM STREET: Reston Intl. Center, 11800 Sunrise Valley Dr., STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 AAAAAALT 22
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100.0%; Pred. No. 1.1;
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                             Query Match
Best Local Similarity
Best Local Similarity
                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-812-421-1
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US-07-812-421-1
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Best Local Similarity
Matches 8; Conserva
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/ACENT INFORMATION:
NAME: Whitham, Michael E.
                                                                                                                                                                                                 TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CITTLECOMMUNICATION INFORMATION:
TELEPHONE: 703-991-2510
TELEFAX: 703-391-9035
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                      STRANDEDNESS:
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STRANDEDNESS:
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15 AAAAAALT 22
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                                          2.3%; Score 8; DB ilarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
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sston_intl. Center, 11800 Sunrise Valley
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/ 100.0%; Pr
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Pred. No.
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                                                             DB 2;
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                                              Gaps
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RESULT 15
US-09-100-664A-2
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Best Local :
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                                                                                                                                                                                                                                         sequence 2, Application US/09100664A Patent No. 6057129
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   APPLICANT:
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

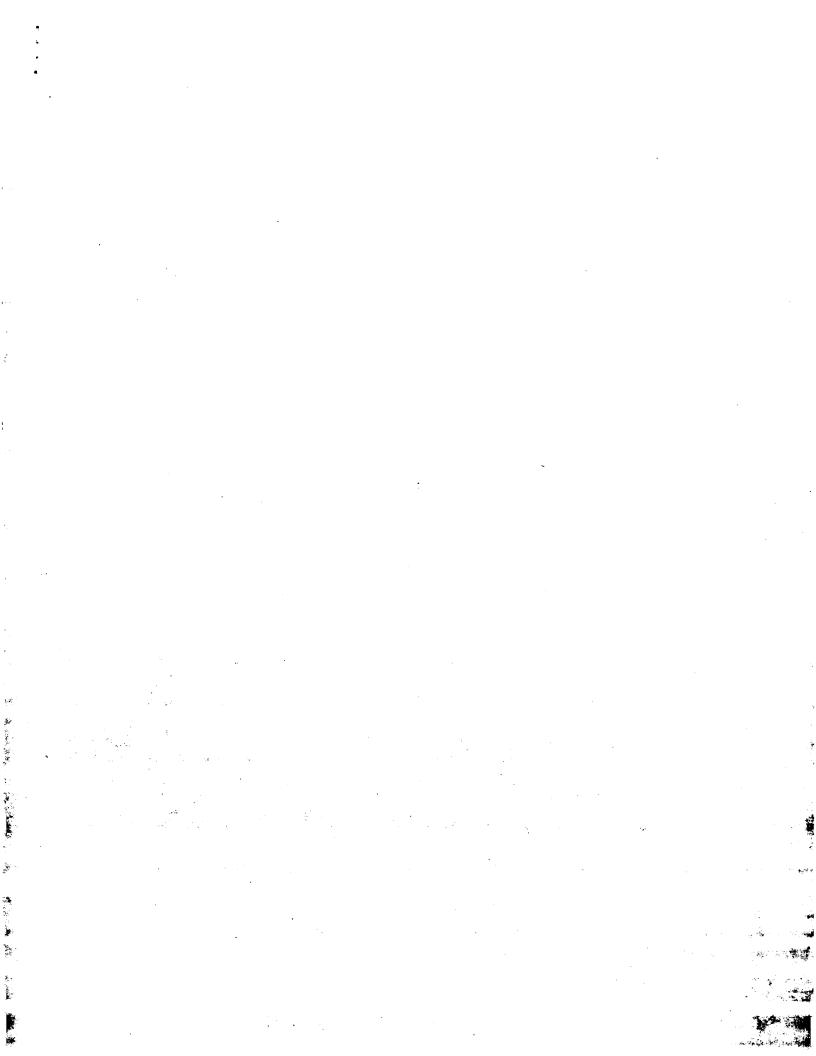
COMPUTER: IBM PC compatible

COMPUTER: IBM PC DOSYMS-DOS

OPERATING SYSTEM: PC-DOSYMS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                         TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 13
                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0153.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: The Board of Trustees of the Leland Stanford Junior APPLICANT: University APPLICANT: Board of Reagents, The University of Texas System TITLE OF INVENTION: Methods and Compositions for Altering TITLE OF INVENTION: Sexual Behavior
                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                           y match 2.3%; Score 8; DB 5; Local Similarity 100.0%; Pred. No. 8.8; es 8; Conservative 0; Mismatches
               STREET: 411 Hacke
CITY: Hackensack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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New Jersey
                                                                                                                                              YOUNG, MICHAEL W. KLOSS, BRIAN BLAU, JUSTIN PRICE, JEFFREY
                                   411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                      Klauber & Jackson
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Search completed: July 11, 2003, 11:07:29 Job time: 27 secs
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Best Local Similarity
""" hes 8; Conserva
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                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION UNMBEF: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                               TOPOLOGY: 11
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FCFM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 440 amine acids
                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 19-JUN
                                                             325 AVAAAAAA 332
                                                                                           13 AVAAAAAA 20
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                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                 600-1-221
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                                                                                                                                     Score 8; Pred. No.
                                                                                                                         Mismatches
                                                                                                                                                   DB 3;
                                                                                                                       0;
                                                                                                                                                  Length 440;
                                                                                                                         Indels
                                                                                                                       0;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB seq length: 0
DB seq length: 2000000000
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349
1 MNIKKTAVKSALAV
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/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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149
152
287
320
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                                                                          0 US-09-864-761-38908

0 US-09-864-761-43779

0 US-10-153-668-2500

US-10-156-761-9684

US-10-156-761-13308

US-10-086-158-6

US-10-086-158-6

US-10-286-264-112

US-09-934-455-304

US-09-934-455-304

US-10-108-605-219

US-10-108-605-219

US-10-108-605-219

US-10-108-605-243

US-10-001-073-44
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US-10-278-173-156
                            US-09-158-180-2
US-10-244-367-44
US-10-229-662-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (without alignments)
26.465 Million cell updates/sec
                                                                                                                        Sequence 250, App
Sequence 9684, Ap
Sequence 13308, A
Sequence 6, Appli
Sequence 112, App
Sequence 112, App
Sequence 199, App
Sequence 199, App
Sequence 219, App
Sequence 243, App
Sequence 243, App
                                          Sequence 44, Appl
Sequence 44, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 44, Appl
           Sequence 2, A
Sequence 2, A
                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                         Sequence 156, App
Sequence 38908, A
Sequence 43779, A
                                                                                                                                                                                                                                                                                                                                                            Sequence 4,
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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US-09-864-761-47806	US-10-219-220-144	US-09-892-877-127	US-09-948-783-128	US-09-738-626-6476	US-09-795-501-10	US-10-106-698-6146	US-09-864-761-40439	US-09-864-761-41747	US-10-106-487-1	US-09-776-724A-165	US-10-311-111-29	US-10-024-450-7	US-10-132-382-4	US-10-132-382-8	US-10-132-382-2	US-10-132-382-6	US-10-108-605-213	US-10-108-605-211	US-08-754-311B-2	US-09-836-392-21	US-09-844-353A-57
Sequence 47806, A	Sequence 144, App	Sequence 127, App	Sequence 128, App	Sequence 6476, Ap	Sequence 10, Appl	Sequence 6146, Ap	Sequence 40439, A	Sequence 41747, A	Sequence 1, Appli	Sequence 165, App	Sequence 29, Appl	Sequence 7, Appli	Sequence 4, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 213, App	Sequence 211, App	Sequence 2, Appli	Sequence 21, Appl	Sequence 57, Appl

ALIGNMENTS

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APPLICANT: MEDITOV, Ruslan
APPLICANT: HORNG, Tiffany
APPLICANT: HORNG, Tiffany
APPLICANT: BARTON, Gregory
TITLE OF INVENTION: TOLL/INTERLEUKIN-1 RECEPTOR ADAPTER PROTEIN (TIRAP)
FILE REFERENCE: 044574-5101US
CURRENT APPLICATION NUMBER: US/10/188,947
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/289,738
PRIOR APPLICATION NUMBER: 60/289,815
PRIOR APPLICATION NUMBER: 60/289,815
PRIOR FILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 12
SEC ID NOS: PatentIn version 3.1
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                                                                               RESULT 2
US-10-278-173-156
: Sequence 156, Application US/10278173
: Publication No. US20030361637A1
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; OTHER INFORMATION: TIRAP polypeptide
US-10-188-947-4
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US-10-188-947-4
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; LENGTH: 241
; TYPE: PRT
; ORGANISM: MUS SP.
; FEATURE:
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                              GENERAL INFORMATION:
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APPLICANT: Jiang, Cai-Zhong
APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
                                                                                                                                                                                                                           279 ASSSSVPASS 288
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pred. No.
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0.29;
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SEQ ID NO 156
LENGTH: 369
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Best Local (
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CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR ADDITOR
                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
FILE REFERENCE: MBI-009
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: Aeomica-X-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                   APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
                                                                                                                 APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
FILING DATE:
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Chen, Wensheng
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Ratcliffe, Oliver
Adam, Luc
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Pilgrim, Marsha
Keddie, James
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                                 2001-01-30
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100.0%; Pred. No.
                PCT/US01/00665
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RESULT 4
US-09-864-761-43779
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                                  PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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LENGTH: 20
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Best Local
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 8; Conserv
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EXPRESSED IN PLACENTA, SIGNAL = 1
EXPRESSED IN LUNG, SIGNAL = 1
EXPRESSED IN HEART, SIGNAL = 1
EXPRESSED IN FETAL LIVER, SIGN
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PCT/US01/00665
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Pred. No. 1.9;
0; Mismatches
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ADULT LIVER, SIGNAL -
BRAIN, SIGNAL - 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
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SOFTWARE: Annomax Sequence
SEQ ID NO 43779
                                      SEQ ID NO
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NUMBER OF SEQ ID NOS: 488
SOFTWARE: Patentin Ver. 2.0
EQ ID NO 250
LENGTH: 152
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MURAMATSU Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
                                                                                                                           PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: JP 2001-313175
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR FILING DATE: 2001-05-25
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACEMTA, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: SWISSPROT HIT: Q09639, EVALUE 3.70e-01
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TYPE: PRT
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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8; Conserv
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100.0%; Pr
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9684
LENGTH: 287
TYPE: PRT
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Best Local Similarity
""+"hes 8; Conserv
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; ORGANISM: Homo
US-10-153-668-250
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US-10-156-761-13308
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APPLICANT: IKEDA, HARJJ
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSSI
APPLICANT: SHIBA, TADAYOSSI
NUMBER OF SEQ ID NOS:
SEQ ID NO 13308
LENGTH: 320
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                                                 CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29 PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30 PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADDYOSHI
APPLICANT: SAKAKI, YOSHYUKI
APPLICANT: HATORI, MASAHYRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                        FILE REFERENCE: 249-262
                                                                                                                                                                    APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                           INFORMATION:
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HORIKAWA, HIROSHI
                                                                                                                                                                                                      SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
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; ORGANISM: Drosophila melanogaster US-10-071-458-4
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TYPE: PRT
ORGANIZM: Drosophila melanogaster
US-10-086-156-6
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US-10-086-156-6
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                                                                     Query Match
Best Local
                                                                                                                                                      SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 338
TYPE: PRT
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Publication No. US20030114371A1
GENERAL INFORMATION:
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APPLICAMT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING
TITLE OF INVENTION: K+betaM4 and K+betaM5
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Best Local
                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 76
                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/071,458
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: US 60/267,039
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/281,224
PRIOR FILING DATE: 2001-04-03
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bristol-myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBU
TITLE OF INVENTION: K+betam3
FILE REFERENCE: D0114.np
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CURRENT APPLICATION NUMBER: US/10/086,156
CURRENT FILING DATE: 2002-02-28
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PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin version 3.0
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                                                 Local Similarity es 8; Conserva
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                 13 AVAAAAAA 20
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28;
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                                               0; Indels
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US-10-286-264-112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/286,264
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 112
LENGTH: 374
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 304, Application US/09934455 Publication No. US20030121070A1
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APPLICANT:
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APPLICANT:
                            CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
                                                                                                                                   APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reuber, Lynne
APPLICANT: Pilgrim, Marsha
APPLICANT: Samaha, Raymond
TITLE OF INVENTION: POLYNUCLEOTIDES FOR SEED TRAIT ALTERATION
FILE REFERENCE: MBI-008
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APPLICANT:
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APPLICANT: Creelman,
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ORGANISM: Arabidopsis thaliana
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               APPLICATION NUMBER: MBI-0023
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Heard, Jacqueline
Jiang, Cai-Zhong
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Riechmann, Jose Luis
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Ratcliffe, Oliver
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Heard, Jacqueline
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Ratcliffe, Oliver
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Query Match
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US-10-108-605-199
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US-10-156-761-12190
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CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-6
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEO ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12190
LENGTH: 427
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SEQ ID NO 304
LENGTH: 374
TYPE: PRT
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Best Local (
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APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
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HORIKAWA, HIROSHI
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nilarity 100.0%;
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100.0%; Pred. No. 32;
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APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kin
FITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MEL
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY A
FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR APPLICATION NUMBER: US 66/176,418
PRIOR FILING DATE: 2001-01-14
NUMBER OF SEQ ID NOS: 361
NUMBER OF SEQ ID NOS: 361
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Best Local Similarity
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US-10-108-605-243
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US-10-108-605-219
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Best Local Similarity 100.
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SEQ ID NO 219
LENGTH: 440
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 243
LENGTH: 440
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CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
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APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kin
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Pred. No.
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o. 38;
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US-10-108-603-243

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Search completed; July 11, 2003, 11:40:17

Job time: 1524 secs
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Post-processing: Minimum Match 0%
Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNIKKTAVKSALAVAAAAAA.....AKGAKVNPNGHKRYRVNFEH
                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
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                                                                                   /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                   SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
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1192.422 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908470
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Pred. No. is the number of results predicted by chance score greater than or equal to the score of the result and is derived by analysis of the total score distribut Pred. No. to have a being printed,

SUMMARIES

Result No.	Score	Query Match Length DB	ength	DB	ID	Description
1	257.5	14.1	308	20	AAW93001	B. alkalophilus be
2	250.5	13.7	242	10	AAP95000	Bacillus subtilis
ω	248	13.6	214	22	AAE07317	Barley recombinant
4	248	13.6	239	1	AAR06621	Hybrid (1,3-1,4)-p
v	229	12.6	208	23	ABB76858	Bacterial lichenas
o	229	12.6	214	23	ABB76859	Bacterial lichenas
7	228	12.5	234	11	AAR03775	Thermostable beta-
8	228	12.5	237	11	AAR05803	Heat-stable endo-b
9	222.5	12.2	237	11	AAR06622	Hybrid (1,3-1,4)-p
10	190.5	10.4	245	19	AAW37884	Lichenase protein.

New Bacillus alkalophilus beta-glucanase protein and gene - useful for removing glucan and/or lichenan from membranes in the brewing industry

Arabidopsis thalia	638	21	0	7.9	144.5	45
Herbicidally activ	179	23	0		14	44
Oerskovia xanthine	945	18	6		145	43
Arabidopsis thalia	035	21	-		45.	42
Herbicidally activ	094	23	-		45.	41
Arabidopsis thalia	036	21	\vdash		45.	40
Arabidopsis thalia	036	21	0			39
Herbicidally activ	385	23	α		45.	38
A. thaliana merist	AAY08308	20	247	8.4	154	37
Protein encoded by	159	18	4		5	36
Oerskovia beta-1,3	736	17	0		54.	35
Herbicidally activ	385	23	œ		154.5	34
Clostridium perfri	806	22	4		15	33
Arabidopsis thalia	032	21	9		56.	32
Arabidopsis thalia	032	21	g		56.	31
Arabidopsis thalia	034	21	0		57.	30
Arabidopsis thalia	265	21	ø		57.	29
Arabidopsis thalia	034	21	9		157.5	28
Herbicidally activ	316	23	σ		57.	27
Arabidopsis thalia	265	21	Φ		57.	26
· Arabidopsis thalia	035	21	σ		57.	25
Arabidopsis thalia	034	21	σ		57.	24
Herbicidally activ	310	23	∞		59.	23
Herbicidally activ	385	23	œ		16	22
Herbicidally activ	310	23	œ		6	21
Arabidopsis thalia	864	21	9		0	20
Herbicidally activ	316	23	œ		170.5	19
Arabidopsis thalia	864	21	æ		0.	18
Arabidopsis thalia	864	21	σ		0.	17
Herbicidally activ	316	23	7			16
Arabidopsis thalia	211	21	7			15
Herbicidally activ	145	23	8		17	14
Arabidopsis thalia	246	21	8		173	13
Herbicidally activ	373	23	8		185	12
Arabidopsis thalia	846	21	æ	0	185	11

ALIGNMENTS

RESULT 1 AAW93001 ID AAW9	IIT 1 ANN93001 standard; Frotein: 308 AA.
AC X	AAW93001;
××	
X DI	19-MAY-1999 (first entry)
XX	B. alkalophilus beta-glucanase protein.
Z X	nase; enzyme; gl
×	Adambmone, took themself, stouting.
× S S	Bacillus alkalophilus.
XX	DE19732751-A1.
X PD	04-FEB-1999.
XX	30-JUL-1997; 97DE-1032751.
XX XX	30-JUL-1997; 97DE-1032751.
XX XX	(HENK) HENKEL KGAA.
ΡI	Hillen W, Maurer K;
DR	WPI; 1999-122161/11.
X R	N-PSDB; AAX02912.
PΤ	New Bacillus alkalophilus beta-glucanase protein a
ŢŢ	ving glucan and/or lichenan from
PT	industry

membrane;

밁 Š 밁 Ş 밁

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RESULT 2
AAP95000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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Best Local
                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                     The lichenase gene from Bacillus subtilis Y-25 is used for transforming Bacillus hosts so that they show increased lexpression. The recombinant lichenase enzyme produced by transformants is useful in beer production for decomposit
                                                                     Sequence
                                                                                            glucan from
                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                 WPI; 1989-119863/16.
                                                                                                                                                                                                                                                                             08-SEP-1987;
                                                                                                                                                                                                                                                                                                                        13-MAR-1989.
                                                                                                                                                                                   Recombinant plasmid used in beer prodn. -
lichenase gene derived from Bacillus subti
                                                                                                                                                                                                                       N-PSDB; AAN95000
                                                                                                                                                                                                                                                                                                    08-SEP-1987;
                                                                                                                                                                                                                                                                                                                                              JP01067181-A
                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis lichenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP95000 standard;
                                                                                                                                                                                                                                                                                                                                                                                                     Beer production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a novel beta-glucanase isolated from Bacillus alkalophilus DSM 9956. This enzyme is useful for removing glucan and/or lichenan from membranes and equipment in the food industry, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                       (ASAK ) ASAHI BREWERIES
                                                                                                                                                                                                                                                                                                                                                                                          Lichenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        brewing industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 DFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Conserv
                                   Similarity
TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTRVQFNYFTNGVG---NNEHYHELGFDASESFNTYAFEWRPESISWYVNGELVYTA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TENIPQTPQKIMMNLWPGIGVDGWTGVFDGEDTPVVTEYDWV---RYTP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYKAGELRTNQFYQYGLFEVNMKPAKSTGTVSSLFTY-TGPWDWDNDPWDEIDIEFLGKD
                                                                     242 AA;
                                                                                                                                                              Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 AA
                                                                                            barley.
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.
                                                                                                                                                                                                                                                                             87JP-0224615
                                                                                                                                                                                                                                                                                                    87JP-0224615
                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gpp;
                                                                                                                                                                                                                                                                                                                                                                                                      fermentation;
                                                                                                                                                              7pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                  13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German.
                                                                                                                                                              Japanese
                                                                                                                                                                                                                                                       즛
                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                      Score 250.5;
Pred. No. 5.8e
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 257.5; DB 20;
Pred. No. 2.1e-13;
2; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                   barley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                                                                                                                                   dn. - obtd. by integrating
subtilis, into vector
                                                                                                                                                                                                                                                                                                                                                                                                   beta-glucan;
                      5.8e-13;
hes 75;
                                            DB 10;
                                                                                                    decomposing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                       Indels
                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                   hydrolysis;
                                                                                                                                        tor
                                                                                                                          lichenase
                                              242;
                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154
                       6
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RESULT 3
AAE07317
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                  carbohydrate present in the barley endosperm. The invention provious barley based foodstuff which comprises a recombinant carbohydrate degrading enzyme improving the nutritional value of the foodstuff The present sequence is barley recombinant, thermostable (1,3-1,4)-beta-glucanase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a food stuff comprising barley feed and transgenic barley malt where the transgenic barley malt comprises a recombinant carbohydrate degrading enzyme comprising a (1,3-1,4)-beta-glucanase. The food stuff is useful to feed animal, preferably chickens Barley is cheaper than corn, the principal foodstuff of chickens. Chickens cannot efficiently utilise barley as an energy source as they do not possess a gut enzyme that depolymerises beta-D-glucan, major carbohydrate present in the barley endosperm. The invention provides a carbohydrate present in the barley endosperm. The invention provides a
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New barley based foodstuff for animals, i.e. chicken comprising recombinant carbohydrate degrading enzyme (1,3-1,4)-beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-497082/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Von Wettstein D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-FEB-2001; 2001WO-US04222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200159141-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1,3-1,4)-beta-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barley; transgenic barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barley recombinant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE07317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE07317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137
                                                 83
                                                                                                52 TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI
                                                                                                                            23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                             Similarity
EFLGKDTTKVQFNYYTNGVGGH----EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VL
                                 EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPT---DGTPWDEIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 37-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHTATNQIPTTPGK--IMMNLWNGTGVDEWLGSYNGVN-PLYAHYDWVRYTK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFLGKDTTKVQFNYYTNGAG----NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                                                                                                                                                                     214 AA;
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0181473
2000US-0247126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thermostable (1,3-1,4)-beta-glucanase enzyme
                                                                                                                                                                                                                             13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malt; carbohydrate
nutritional value;
                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horvath
                                                                                                                                                                                                                       Score 248; DB 2
Pred. No. 8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                   70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    degrading enzyme; chicke foodstuff; thermostable.
                                                                                                                                                                                                                                               Length 214;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chicken;
                                                                                                                                                                                                   Gaps
                                                                                                108
                                                                                                                                                 82
164
                                                 142
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AAR06621
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                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                      This hybrid protein is encoded by the beta-glucanase-H1 gene. Following processing of the signal peptide the mature protein is produced, comprising the amino terminus of the amylolique-faciens beta-glucanase and the carboxyl-terminal half of the B.maccarans beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glycosidic linkages in (1,3-1,4)-beta-glucanase Reducing sugars are obtd. at high temps. and thus this enzyme can be used in the mfr. of food prods., esp. beer and animal feed (eg. for feeding sugars are obtd.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New thermostable (1,3-1,4)-beta-glucanase - gene obtd. using Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-1989;
16-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR06621 standard;
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-275129/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CARL-) CARLSBERG A/S (DEAK ) AKAD WISSENSCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9009436-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                        feeding
                                         134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
   143
                                                                             83
                                                                                                                   77
                                                                                                                                                       23
                                                                                                                                                                                             l Similarity
62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pre-beta-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1,3-1,4)-pre-beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             æ
 RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                                                                                                                                     TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHT---ATANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT 212
                                     EFLGKDTTKVQFNYYTNGVGGH----EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VL
                                                                         EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                 TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amyloliquefaciens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT
                                                                                                                                                                                                                                                                         239 AA;
                                                                                                                                                                                                                                                                                                          poultry).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    page 26; 84pp;
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WISSENSCHAFT DDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89DK-0003848.
89DD-0325800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90WO-DK00044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=amino terminal of 133..236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ∕label=carboxyl-terminal of B.macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                             13.6%;
                                                                                                                                                                                                                                                                                                          See also AAQ05833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ç
                                                                                                                                                                                           27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucans; beer; animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomsen KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239
                                                                                                                                                                                         Score 248; DB 11;
Pred. No. 9.3e-13;
7. Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepd. using hy and B.macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ó
                                                                                                                                                                                                                             Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      feed;
                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybrid
                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes
                                                                                                                                                                                         Gaps
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RESULT 6
ABB76859
ID ABB7
XX
AC ABB7
AC ABB7
XX
DT 27-J
XX
DE Bact
XX
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ABB76 ABB7 ABB77 XX
AC ABB7
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AC ABB7
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AC ABB7
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                   Bacterial lichenase
                                                         27-JUN-2002
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Query Match
Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a protein sequence from a soil bacterium enzyme with lichenase/endo-1,3/1,4-beta-glucanase (E.C. 3.2.1.73 activity. The enzyme is useful in brewing and for degrading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
ABB76859 standard; Frotein;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-glucanases that cause problems during filtration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Page 18-19; 27pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing nucleic acid encoding lichenase, useful for producing enzymes for improving filtration in brewing, comprises isolating the nucleic acid from soil bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200212511-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soil bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial lichenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB76858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB76858 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodriguez Munoz V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000ES-0001922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-217195/27
                                                                                                                              143
                                                                                                                                                                     112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 KHT---ATANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT
                                                                                           168
                                                                                                                                                                                                        83
                                                                                                                                                                                                                                           55
                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL53374.
                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                   EFLGKDTTKVQFNYYTNGAG---NHEKLADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L 167
                                                                                                                                                                                                                                                                 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                             TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI
                                                                                                                                                                                           EVLGKNPGSFCSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                         KHTATTQIPAAPGK--IMMNLWNGTGVDDWLGSYN
                                                                                                                              RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   soil bacteria
                                                                                                                                                                                                                                                                                                                                                                                                208
                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme; lichenase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perez Mellado R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                       12.6%;
36.1%;
                                                                                                                                                                                                                                                                                                                      22;
 214
                                                                                                                                                                                                                                                                                                                                     Score 229; DB 2
Pred. No. 3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endo-1,3/1,4-beta-glucanase; brewing.
                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                      67;
                                                                                           200
                                                                                                                                                                                                                                                                                                                                                       Length 208;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                    Gaps
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(first entry)

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RESULT 7
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Best Local
                                                                                                                                                                                                                                                                                                            Matches
                                                                                       Bacillus macerans.
                                                                                                        Thermostable
                                                                                                                                                                                                                                                                                                                                                         The present sequence is a protein sequence from a soil bacterium for enzyme with lichenase/endo-1,3/1,4-beta-glucanase (E.C. 3.2.1.73) activity. The enzyme is useful in brewing and for degrading beta-glucanases that cause problems during filtration.
                                                                                                                                                                                                                                                                                                                                                                                                                Producing nucleic acid encoding lichenase, useful for producing enzymes for improving filtration in brewing, comprises isolating the nucleic acid from soil bacteria .
          (DEAK ) AKAD
                                         12-MAY-1988;
                                                                         DD272102-A.
                                                                                                                       Thermostable beta-glucanase
                                                                                                                                        31-JUL-1990
                                                                                                                                                        AAR03775;
                                                                                                                                                                       AAR03775 standard;
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 21-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABL53375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodriguez Munoz V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUL-2001; 2001WO-ES00303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200212511-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                         12-MAY-1988;
                                                         27-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000; 2000ES-0001922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soil bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-217195/27.
                                                                                                                                                                                                               173
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                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                          56; Conserv
                                                                                                                                                                                                               KHTATTQIPAAPGK--IMMNLWNGTGVDDWLGSYN 205
                                                                                                                                                                                                                              RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFD 176
                                                                                                                                                                                                                                             EFLGKDTTKVQFNYYTNGAG----NHEKLADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L
                                                                                                                                                                                                                                                            EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                                                                                                                                                                                                          214 AA;
                                                                                                                                                                                                                                                                                                            Conservative
          WISSENSCHAFT DDR
                                                                                                                                       (first entry)
                                                                                                        beta-glucanase;
                          88DD-0315706
                                         88DD-0315706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzyme; lichenase; endo-1,3/1,4-beta-glucanase; brewing
                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perez
                                                                                                                                                                                                                                                                                                                   12.6%;
                                                                                                                                                                                                                                                                                                                                                                                                27pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mellado
                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                       234
                                                                                                        SS;
                                                                                                                                                                                                                                                                                                                   Score 229;
Pred. No. 3.
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                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                        Bacillus
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es 67;
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                                                                                                        subtilis
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                                                                                                                                                                                                                                                                            116
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                                                                                                                                                                                                                                                                                    RESULT 8
AAR05803
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
The corresp. gene and the plant promoter region are inserted into expression vector and used to transform barley cells. The transform used to regenerate barley plants which are useful in brewing.
                                                                                                                                                                       31-JAN-1990
                                                                                                                                                                                       DD275704-A.
                                                                                                                                                                                                                                                     08-NOV-1990
                                                                                                                                                                                                                                                                     AAR05803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mashes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macerans.
                                                                                                                                        23-SEP-1988;
                                                                                                                                                       23-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borriss
                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                          143
                                                                                                                                                                                                                                                                                                                                                           129
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                                                                                                                                                                                                                                                                                                                                                                                         72
                                                                                                                                                                                                                                                                                                                                                                                                                        60;
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Prepn. of barley plants expressing heat stable beta-glucanase -
by transforming cells with appropriate vector then regeneration
giving seeds useful in brewing without conversion to malt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-glucanase is expenzyme is useful for
Disclosure; ; p; German.
                                                                                                                           WPI; 1990-210631/28.
N-PSDB; AAQ05167.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endo-beta-1,3-1,4-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat-stable endo-beta-1,3-1,4-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR05803 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermostable beta-glucanase production - using Bacillus subtilis transformed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-067913/10.
N-PSDB; AAQ03519.
                                                                                                                                                                                                                                (DEAK ) AKAD WISSENSCHAFT DDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 1; ; 9pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHT---ATANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFLGKDTTKVQFNYYTNGVGGH---EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the production of feedstuff
                                                                                                                                                                                       Wobus U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                            88DD-0320082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed in Bacillus subtilis. The for lowering the viscosity of brewing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.5%;
                                                                                                                                                                                            Mendel R-R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 228; DB 11;
Pred. No. 4.3e-11;
5; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     barley; brewing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                          Baumlein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thermostable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234;
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Best Local :
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        This hybrid protein is encoded by the beta-glucanase-H2 gene. Following processing of the signal peptide the mature protein is produced, comprising the amino terminus of the B.macerans beta-glucanase and the carboxyl-terminal half of the B.amylo-liquefaciens beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glycosidic linkages in (1,3-1,4)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein accumulates proportion of these
                                                                                                                New thermostable (1,3-1,4)-beta-glucanase - gene obtd. using Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                 04-AUG-1989;
16-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
beta-glucans.
                                                                                            Disclosure;
                                                                                                                                                                                                            (CARL-)
(DEAK )
                                                                                                                                                                                                                                                                                   16-FEB-1990;
                                                                                                                                                                                                                                                                                                          23-AUG-1990
                                                                                                                                                                                                                                                                                                                                WO9009436-A
                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR06622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unacceptable increase in viscosity.
                                                                                                                                                    1990-275129/36
DB; AAQ05833.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          pre-beta-glucanase; glucans; beer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1,3-1,4)-pre-beta-glucanase
                                                                                                                                                                                      ₽,
                                                                                                                                                                                                              AKAD
                                                                                                                                                                                                                          CARLSBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    amyloliquefaciens, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHT---ATANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFLGKDTTKVQFNYYTNGVGGH----EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237
                                                                                           page
                                                                                                                                                                                      Hofemeister J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                            WISSENSCHAFT DDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ulates in the ripe (but ungerminated) seeds. The these to malted seeds is increased therefore, without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
Reducing sugars
                                                                                                                                                                                                                                                89DK-0003848
89DD-0325800
                                                                                                                                                                                                                                                                                 90WO-DK00044
                                                                                                                                                                                                                                                                                                                                                              /label=carboxyl-terminal half of B.amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                             /label=amino-terminal half of B.macerans beta-glucanase 131..234
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                          A/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.5%;
                                                                                         84pp; English.
                                                                                                                                                                                                                                                                                                                                                      beta-glucanase
                                                                                                                                                                                      Thomsen
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Pred.
are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228; DB 11;
No. 4.4e-11;
obtd.
                                                                                                                                                                                     KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                     macerans
at high temps. and
                                                                                                                                                                                      Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                           animal feed; poultry.
                                                                                                                  prepd. using hybrid
and B.macerans gene
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                                                                                                                                                                                      Vonwettstein
                                                                                                                 genes
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
      This sequence is the lichenase (licA) of Orpinomyces sp. strain PC-2 of the invention. The protein was purified from a fungus or a fungal culture or from a recombinant DNA molecule having a fungal lichenase coding sequence. The lichenase enzyme hydrolyses the beta-1,4-glucan bonds adjacent to beta-1,3-linked glucan bonds, but does not cleave beta-1,4-linked glucans. They can be used for the treatment of animal beta-1,4-linked glucans. They can be used for the treatment of animal beta-1,4-linked glucans.
                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-1,3-linked nutrient availab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thus this enzyme can beer and animal feed AAQ05833.
                                                                                       Claim 1; Page 24-25; 41pp; English.
                                                                                                                                                                                                Chen H,
                                                                                                                                                                                                                                               04-OCT-1996;
                                                                                                                                                                                                                                                                      03-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                              Orpinomyces sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                            used for treatment of grain
                                                                                                                                      New isolated lichenase protein
                                                                                                                                                                                                                        (UYGE-)
                                                                                                                                                                                                                                                                                            09-APR-1998
                                                                                                                                                                                                                                                                                                                   WO9814595-A1
                                                                                                                                                                                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW37884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW37884 standard;
                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lichenase;
                                                                                                                fermentation processes
                                                                                                                                                                         1998-240094/21
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                                                                                                                                                              AAV29067
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                                                                                                                                                                                                                                                                                                                                                                                                                                     availability;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHTATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYHWMRYRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                            licA;
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                                                                                                                                                                                                                                                                                                                                                   /note=
30..246
                                                                                                                                                                                                                                                                                                                                                                                                                                               glucan
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                        RES
                                                                                                                                                                                                                                                                                                                                                    246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%;
33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used in the mfr. of food (e.g.for feeding poultry).
                                                                                                                                                                                                                                                                                                                                                                                                                                is; enzyme; beta-1,4-glucan bond hydrolysation;
bond; grain-containing feed; grain treatment;
brewing; fermentation.
                                                                                                                                                                                                                                                                                                                                                              "signal peptide
                                                                                                                                                                                                                                                                                                                                        "mature lichenase"
                                                                                                                                                                                                                      FOUND
                                                                                                                                                                                                ۲e;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
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Pred. No. 1.3e-10;
Pred. No. 1.3e-10;
                                                                                                                            improve feeds
                                                                                                                                          •
                                                                                                                                                                                                                        INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA
                                                                                                                                       is obtained
                                                                                                                            from Orpinomyces PC-2, or to improve brewing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See
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                                                                                                                           brewing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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RESULT 11
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54; Conservative
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99US-0128724

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99US-0130477

99US-013049

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; Pred. No. 6.5e-08;
17; Mismatches 87;
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12-AUG-1999; 13-AUG-1999; 13-AUG-1999; 16-AUG-1999; 17-AUG-1999;

10-AUG-1999; 11-AUG-1999;

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RESULT 12
ABB93737
ID ABB93
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26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                 The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -
                                                                                                                                                                                                                                                     Claim
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                          herbicides
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99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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S-0145951. S-0146386. S-0146388. 3-0146389. 3-0147038.

5-AUG-1999; 5-AUG-1999; 5-AUG-1999;

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The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from pla with nucleic acid or amino acid sequences from non-plant organisms witable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant
                                                                                                                                                                                                                Identifying plant target comprising aligning and of from plant with nucleic a
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23-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
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Similarity 25.6%;
64; Conservative 3
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99US-012548
99US-0125788
99US-0126785
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99US-0130510
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Pred. No. 2.3e
36; Mismatches
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promoter;
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Similarity 26.6%;
54; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                GQEVRKTEGGQVSNLTGTQGLRF------NLWSSESAAWVG---QFDESKLPLFQF | :|: | :| | | | | : | | | : | | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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990S-0160980.
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990S-0161405.
990S-0161406.
990S-0161350.
990S-0161350.
990S-0161351.
990S-0161920.
990S-0161920.
990S-0161923.
                           11,
                                                                                                                                  WKVYKYTPGQGE 200
                           2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                           10:52:52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 172.5;
Pred. No. 2.5e
34; Mismatches
                                                                                                    235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB .
2.5e-06;
3s 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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138

158

81

9;

101

185

212

22-JUL-1999
23-JUL-1999
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24-JUL-1999
27-JUL-1999
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